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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:15:18 ; Search time 58.56 Seconds  
(without alignments)  
1126.671 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHGASVGYQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 747574 seqs, 111073796 residues 747574  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3019	100.0	594	20 AAY23740	A surface protein
2	3019	100.0	594	21 AAY57044	BASB029 amino acid
3	3019	100.0	594	22 AAU06174	N. meningitidis EG
4	2874	95.2	594	20 AAY23739	A surface protein
5	2874	95.2	594	22 AAU06179	N. meningitidis BZ
6	2855	94.6	598	20 AAY23742	A surface protein
7	2855	94.6	598	22 AAU06177	N. meningitidis H1
8	2852	94.5	598	20 AAY23738	A surface protein
9	2852	94.5	598	22 AAU06178	N. meningitidis BZ
10	2783.5	92.2	591	21 AAY57045	BASB029 amino acid
11	2762.5	91.5	599	20 AAY23743	A surface protein

12	2762.5	91.5	599	22 AAU06176	N. meningitidis H3
13	2758.5	91.4	591	20 AAY27202	Amino acid sequenc
14	2758.5	91.4	591	20 AAY23746	A surface protei
15	2758.5	91.4	591	22 AAU06171	N. meningitidis PM
16	2751	91.1	592	20 AAY23737	A surface protein
17	2739.5	90.7	591	20 AAY23741	A surface protein
18	2739.5	90.7	591	22 AAU06175	N. meningitidis EG
19	2636	87.3	592	20 AAY23744	A surface protein
20	2636	87.3	592	22 AAU06172	N. meningitidis H4
21	2533	83.9	592	22 AAU06180	N. meningitidis Z2
22	2516.5	83.4	589	20 AAY23745	A surface protein
23	2516.5	83.4	589	22 AAU06173	N. meningitidis P2
24	2504	82.9	592	20 AAY27203	Amino acid sequenc
25	2449	81.1	512	22 AAU06182	N. meningitidis PM
26	2409.5	79.8	513	22 AAU06183	N. meningitidis H4
27	2366	78.4	502	22 AAU06186	N. meningitidis PM
28	2230	73.9	604	22 AAU06185	N. meningitidis su
29	2032.5	67.3	433	22 AAU06185	N. meningitidis PM
30	1887.5	62.5	407	22 AAU06184	N. meningitidis PM
31	1328.5	44.0	2353	17 AAR99393	Haemophilus adhesi
32	1292.5	42.8	2411	21 AAB23860	Haemophilus influe
33	1055	34.9	1094	21 AAB23858	Haemophilus influe
34	1050	34.8	245	20 AAY27201	Amino acid sequenc
35	1030	34.1	1098	17 AAR99392	Haemophilus adhesi
36	978.5	32.4	679	17 AAR99394	Haemophilus adhesi
37	978.5	32.4	679	21 AAB23855	Haemophilus influe
38	741	24.5	1004	21 AAB23857	Haemophilus influe
39	727	24.1	1002	21 AAB23854	Haemophilus influe
40	689	22.8	1104	21 AAB23856	Haemophilus influe
41	689	22.8	1104	21 AAB23859	Haemophilus influe
42	595	19.7	116	21 AAB37832	Neisserial conserv
43	394.5	13.1	2314	22 AAB69136	M. catarrhalis les
44	393.5	13.0	1992	17 AAW04505	Moraxella 200 kDa
45	393.5	13.0	1992	22 AAB69133	M. catarrhalis str

ALIGNMENTS

RESULT 1  
AAY23740  
ID AAY23740 standard; Protein; 594 AA.  
XX  
AC AAY23740;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85792.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX

PS	Claim 1; Page 100-101; 132pp; English.
XX	
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for
CC	the detection or diagnosis of N. meningitidis infection in humans.
CC	The N. meningitidis surface glycoproteins can also be used to
CC	prevent or treat N. meningitidis infection in humans, especially
CC	in the form of vaccines. The proteins and antibodies can also
CC	be used to identify immunoreactive peptides.
XX	
SQ	Sequence 594 AA;
Query Match 100.0%; Score 3019; DB 20; Length 594;	
Best Local Similarity 100.0%; Pred. No. 5.1e-173;	
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	
QY	1 mnkiyriiwnsalnawvavseltrnhtrkrasatvatavlatllfatvqasttdddllyle 60
Db	
QY	61 PVQRTAVVLSFRSDKEGTGEKVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
Db	
QY	61 pvqrtavvlsfrsdkegtgekevtedsnwgvfyfdkkgvltagtitlkagdnlkikqntne 120
QY	121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNPAKKTAEETNGDTTVH 180
Db	
QY	121 ntnassfty slkkdltdltsvgtelksfsansknvnitstdtkglnfakktaeetngdttvh 180
QY	181 LNGIGSFLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240
Db	
QY	181 lngigstltdtllntgattntvndnvtdddkkraasvkdvl Nagwnikgvpkpgttasdnv 240
QY	241 DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGKLVTKDKKGEND 300
Db	
QY	241 dfvrttydtveflsadtktttvnnveskdngkrtevkigaktsvikekdgklvtgdkgend 300
QY	301 SSTDKGGLVTAKEVIDAVNKAGWRMKTTTANGTGQADKFETVTSNTVFASGKGTTA 360
Db	
QY	301 sstdkgglvtakevidavnkagwrmttttangtgqadkfetvtsntvtfasgkgtta 360
QY	361 TVSKDDQGNITVMYDYNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
Db	
QY	361 tvskddqgnitvm yd ynvvgdalnv nqlqns gwnldskavagssgkvisgnvpskgkmd 420
QY	421 TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDANK 480
Db	
QY	481 PVRITNVAPGVKEGDTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPG 540
Db	
QY	481 pvr itnvapgvkegdtnvaqlkgvaqnlnh idnv dngdnarag iaqiaataglvqaylpg 540
QY	541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
Db	
QY	541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594
RESULT	2
AAAY57044	
ID	AAAY57044 standard; Protein; 594 AA.
XX	
AC	AAAY57044;
XX	
DT	21-FEB-2000 (first entry)
XX	
DE	BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
XX	
KW	BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW	infection; treatment; prevent; antibacterial drug.
XX	

OS	Neisseria meningitidis.
XX	
EH	Key Location/Qualifiers
FT	Misc-difference 104
FT	/note= "Encoded by AATC"
XX	
PN	WO9958683-A2.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-EP03255.
XX	
PR	13-MAY-1998; 98GB-0010276.
XX	
PA	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX	
PI	Ruelle J;
XX	
DR	WPI; 2000-053103/04.
DR	N-PSDB; AAZ39864.
XX	
PT	New polypeptide from neisseria meningitidis useful for diagnosis,
PT	treatment or prevention of bacterial infections in mammal
XX	
PS	Claim 4; Fig 2; 74pp; English.
XX	
CC	This is the Neisseria meningitidis BASB029 amino acid sequence from
CC	serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC	Haemophilus influenzae surface fibril (HSF) protein. The invention
CC	relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC	polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC	BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC	meningitidis infection in a mammal. Compositions containing an immune
CC	polynucleotides and polypeptides are useful for generating an immune
CC	response in an animal. A therapeutic composition comprising an antibody
CC	directed against BASB029 is useful in treating humans with Neisseria
CC	meningitidis disease. The polynucleotide is useful in the diagnosis of
CC	the stage of infection, type of infection, susceptibility to an
CC	infection which results from increased or decreased expression of the
CC	polynucleotide, and for therapeutic or prophylactic purposes,
CC	particularly genetic immunisation. Antibodies against BASB029
CC	polynucleotides and polypeptides are also useful for treating infections
CC	particularly bacterial infections. The protein is useful in the
CC	screening and development of antibacterial drugs. Fused recombinant
CC	protein is useful for the stimulation of the immune system of an organism
CC	receiving the protein.
XX	
SQ	Sequence 594 AA;
Query Match 100.0%; Score 3019; DB 21; Length 594;	
Best Local Similarity 100.0%; Pred. No. 5.1e-173;	
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	
QY	61 PVQRTAVVLSFRSDKEGTGEKVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
Db	
QY	61 pvqrtavvlsfrsdkegtgekevtedsnwgvfyfdkkgvltagtitlkagdnlkikqntne 120
QY	121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNPAKKTAEETNGDTTVH 180
Db	
QY	121 ntnassfty slkkdltdltsvgtelksfsansknvnitstdtkglnfakktaeetngdttvh 180
Db	
QY	181 LNGIGSFLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240
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QY	181 lngigstltdtllntgattntvndnvtdddkkraasvkdvl Nagwnikgvpkpgttasdnv 240
QY	241 DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGKLVTKDKKGEND 300
Db	
QY	241 dfvrttydtveflsadtktttvnnveskdngkrtevkigaktsvikekdgklvtgdkgend 300
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RESULT 3
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX AC AAU06174;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain EG327.
XX FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
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FT Region 117..126
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FT /note= "Conserved region 5"
XX WO200155182-A1.
XX PD 02-AUG-2001.
XX XX 25-JAN-2001; 2001WO-AU00069.
XX PR 25-JAN-2000; 2000US-0177917.
XX XX
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PA (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
PI
XX WPI; 2001-488774/53.
DR N-PSDB; AAS09164.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 9lpp; English.
PS
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA;

Query Match 100.0%; Score 3019; DB 22; Length 594;
Best Local Similarity 100.0%; Pred. No. 5.le-173;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 mnkiyriiwsalnawvavseltrnhtrkrasatvatavlatllfatvqasttdddlyle 60
QY 61 PVQRTAVVLSFRSDKEGTGEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
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QY 181 LNGIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNV 240
Db 181 lngigstltdlntgattnvtndnvtddekkraasvkdvlnagwnikgvpkpgttasdnv 240
QY 241 DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTGDKGEND 300
Db 241 dfvrt ydtveflsadtktttvnveskdngkrtevkigaktsvikekdglvtgdkgend 300
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVTFASGKGTTA 360
Db 301 sstdkgeglvtakevidavnkagwrmktttangqtgqadkfkfetsgntvtfasgkgtta 360
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QY 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNHIDNVGNARAGIAQAIATAGLVQAYLPG 540
Db 481 pvr itnvapgvkegdvntvaqlkgvaqnlhnhidnvdgnaragiaqaiataglvqaylpg 540
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 594
Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrgrhfgasasvgyqw 594
```



PR 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
PA  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI; 2001-488774/53.  
DR N-PSDB; AAS09169.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain Bz198 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 594 AA;

Query Match 95.2%; Score 2874; DB 22; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.5e-164;  
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Db 481 pvr itnvapgvkegdvtnvaqlkgvaqnl nhr idnvdgnarag iaqaiataglvqaylpg 540

QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVG YQW 594  
Db 541 ksmmaigddtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 6  
AAY23742  
ID AAY23742 standard; Protein; 598 AA.  
XX  
AC AAY23742;  
XX 08-SEP-1999 (first entry)  
XX A surface protein of Neisseria meningitidis.  
DE  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX Neisseria meningitidis.  
XX WO9931132-A1.  
PN  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85794.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 108-110; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 598 AA;

Query Match 94.6%; Score 2855; DB 20; Length 598;  
Best Local Similarity 94.6%; Pred. No. 3.4e-163;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60  
Db 1 mnkiyriiwnsalnawvvvseltrnhtkrasatvatavlatllfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEKTEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdkegtgedswnwavyfdekrvlgagaitlkagdnlkikqntne 120

QY 121 NTNA----SSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGD 176  
Db 121 ntntndssftyssllkdltdltsveteklsfgangknvnitsdtkglnfaketagngd 180

QY 177 TTVHLNIGIGSTLTD TLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKIGVKPGTTA 236  
Db 181 ptv hlngigstltdtllntgattnvtndnvtdddkkraasvkdvl nagwnikgvpgtta 240

QY	237	SDNVDFVRTYDTVEFLSADTKTTTTNVNESKDNKGRTEVKIGAKTSV7KEKGDKLVTGDK	296
Db	241	sdnvdfvrtYdtveflsadtktttvnveskdnkkvckigaktsv7ikekdgklvtgk	300
QY	297	GENDSSTDKGEGLVTAKEVIDAVNRAGWRMKTTTTANGOTGOADKFFETVTSGTNTVFASGK	356
Db	301	dengsstdegeglvtakevidavnkagwrmtttangtggadkfcvtsgtkvtfasgn	360
QY	357	GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSKAVAGSSGKVISGNVSPSKG	416
Db	361	gttatvskddqgnitvmydvnvvgdalnvngqlnsgwnldskavagsgkvisgnvpskg	420
QY	417	KMDETVINAGNNIETRNGKNIDIATSMTPQFSSVSLGAGADAP7LSVDDEGALNVGSK	476
Db	421	kmdetvinagnnieitrngknidiatsmtpfssvslgagadap7lsvddegalnvsgsk	480
QY	477	DANKPVRITNVPVKEGDVTNVAOLKGVAQN7LNHIDNVNVDGNARAGIAQA7IATAGLVQA	536
Db	481	dankpvr7itnvapvkegdvtnvaqlkgvaqnl7nr7idnv7dgnarag7iaq7iatag7laga	540
QY	537	YLPKGSMMAIIGGGTVRGEAGYAIGYSSISDGGNWI7KGTASGNSRHF7GASASVGIQW	594
Db	541	ylpkgsmma7i7gggtvrgeag7y7ig7yss7isdgg7nw7i7kgt7as7ns7rh7f7gas7as7v7gi7qw	598

PF XX PR XX PA XX PI XX DR DR XX PT PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC XX SQ

WO200155182-A1.

02-AUG-2001.



Db 481 dankpvrtnvapgvkegdvtnvaqlkgvaqnlnnrldnvdgnaraglaqaiataglaqa 540

QY 537 YLPGKSMMALGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594

Db 541 ylpgksmmaigggtyrgeagyalgysslsdtgnwvikgtasgnsrghfgasasvgyqw 598

RESULT 8

AAU06178

ID AAY23738 standard; Protein; 598 AA.

XX

AC AAY23738;

DT 08-SEP-1999 (first entry)

XX

DE A surface protein of Neisseria meningitidis.

XX

KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

XX

OS Neisseria meningitidis.

XX

PN WO9931132-A1.

XX

PD 24-JUN-1999.

XX

PF 14-DEC-1998; 98WO-AU01031.

XX

PR 12-DEC-1997; 97GB-0026398.

XX

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU ) UNIV QUEENSLAND.

XX

PI Jennings MP, Moxon ER, Peak IRA;

XX

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85790.

XX

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX

PS Claim 1; Page 91-93; 132pp; English.

XX

CC The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.

CC The N. meningitidis surface glycoproteins can also be used to

CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

XX

SQ Sequence 598 AA;

Query Match 94.5%; Score 2852; DB 20; Length 598;

Best Local Similarity 94.6%; Pred. No. 5.2e-163;

Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60

Db 1 mnkisriiwnsalnawvvseltrnhtkrasatvatavlallfatvganatdddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120

Db 61 pvqrtavvlsfrsdkegtgekgtdsnwavyfdekrvfkagaitlkagdnlkikqntne 120

QY 121 NTNA---SSFTYSLKKDLTDLTSVGTKEKLSFSANSKNVNITSDTKLNFAKKTAEKNGD 176

Db 121 ntntentndssfyslkkdldtltsveteklslfgangknvnitsdtkgnlfaketagtngd 180

QY 177 TTVHLNGIGSTLTDTLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236

Db 181 ptvhlngigstltdtllntgattntndnvtddekkraasvkdvlnagwnikgvkpgtta 240

QY 237 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKRTVEVKIGAKTSVKEKDGKLVTKGDK 296

Db 241 sdnvdfvrydytveflsadtktttvnveskdngkrtevkigaktsvikekdgklvtgk 300

QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRMKTTTTANGQTGOADKFPETVTSCTNVTFASGK 356

Db 301 gengsstdegeglvtakevidavnkagwrmktttangqtgqadkfetvtsgtkvtfasgn 360

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416

Db 361 gttatvskddqgnitvkydvnvgdnlvnqlqnsqwnldskavagssgkvisgnvpskg 420

QY 417 KMDETVINAGNNIEITRNGKNIDIAATMTQFSSVSLGAGADAPTLSVDDEGALNVGSK 476

Db 421 kmdetvinagnnieitrngknidiatsmtqpfssvslgagadaptslsvdddegalnvg 480

QY 477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAIATAGLVQA 536

Db 481 dankpvrtnvapgvkegdvtnvaqlkgvaqnlnnrldnvdgnaraglaqaiataglaqa 540

QY 537 YLPGKSMMALGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594

Db 541 ylpgksmmaigggtyrgeagyalgysslsdtgnwvikgtasgnsrghfgtsasvgyqw 598

RESULT 9

AAU06178

ID AAU06178 standard; Protein; 598 AA.

XX

AC AAU06178;

XX

DT 24-OCT-2001 (first entry)

XX

DE N. meningitidis Bz10 surface antigen Nhha polypeptide sequence.

XX

KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX

OS Neisseria meningitidis strain BZ10.

XX

FH Key Location/Qualifiers

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..104

FT /label= V1

FT /note= "Variable region 1"

FT Region 105..116

FT /label= C2

FT /note= "Conserved region 2"

FT Region 117..130

FT /label= V2

FT /note= "Variable region 2"

FT Region 131..194

FT /label= C3

FT /note= "Conserved region 3"

FT Region 195..216

FT /label= V3

FT /note= "Variable region 3"

FT Region 217..235

FT /label= C4

FT /note= "Conserved region 4"

FT Region 236..242

FT /label= V4

FT /note= "Variable region 4"

FT Region 243..598

FT /label= C5

FT /note= "Conserved region 5"

XX

PN WO200155182-A1.

XX

PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI; 2001-488774/53.  
DR N-PSDB; AAS09168.  
XX  
PT New Nhba surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 9lpp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain Bz10 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 598 AA;

Query Match 94.5%; Score 2852; DB 22; Length 598;  
Best Local Similarity 94.6%; Pred. No. 5.2e-163;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNsALNAwVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 mnkisriiwnsalnawvvvseltrnhtkrasatvatavlatilfatvganatdddldyle 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdkegtgekgtdsnwavyfdekrvllkagaitllkagdnllkikqntne 120  
QY 121 NTNA----SSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAEINGD 176  
Db 121 ntntentndssftyssllkddlttsveteklsfgangknvnitsdtkglnfaketagtngd 180  
QY 177 TTVHLNGIGSLTDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPGTGA 236  
Db 181 ptvhlngigstltdtllntgatntvndnvtdddekkraasvkdvlalnagwnikgvkpgtta 240  
QY 237 SDNVDFVRTYDTEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTKGDK 296  
Db 241 sdnvdfvrtvteflsadtktttvnveskdngkrtevkigaktsvikekdgklvtgkgk 300  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTATTANGOTGOADKFFETVTSGTNVTFASGK 356  
Db 301 gengsstdegeglvtakevidavnkagwrnktttangqtgqadkfetvtsgtkvtfasgn 360  
QY 357 GTTATVSKDDQGNITVMYDVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 416  
Db 361 gttatvskddqgnitvkydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskg 420  
QY 417 KMDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLTSLVDDGALNVGSK 476  
Db 421 kmdetvinagnieitrngknidiatsmtppqfssvslgagadaptlsvddegalnvgsk 480

QY 477 DANKPVRITNVAPGVKEGDVTNVQAQLKGVQONLNNHIDNVGNARAGIAQAIAATAGLVQA 536  
Db 481 dankpvrnitnvapgvkegdvtnvvaqlkgvaqlnnridnvgdnaragiagataglaqa 540  
QY 537 YLPGKSMMAICGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVGYQW 594  
Db 541 ylpgksmmaiaggtyrgeagyaigyssisdgtgnwnvikgtasgnsrghfgtsasvgyqw 598  
RESULT 10  
AAAY57045  
ID AAAY57045 standard; Protein; 591 AA.  
XX  
AC AAAY57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
FH Key Location/Qualifiers  
FT Misc-difference 90 /note= "Encoded by AAT"  
FT Misc-difference 92 /note= "Encoded by GAT"  
FT Misc-difference 98 /note= "Encoded by AAC"  
FT Misc-difference 108 /note= "Encoded by AATC"  
FT Misc-difference 123 /note= "Encoded by ACA"  
FT Misc-difference 269 /note= "Encoded by AAA"  
FT Misc-difference 389 /note= "Encoded by CGT"  
XX  
PN WO9558683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39865.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
XX treatment or prevention of bacterial infections in mammal  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
CC polypeptide sequences (AAAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing a Neisseria  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BasB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the



CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 92.2%; Score 2783.5; DB 21; Length 591;  
Best Local Similarity 93.3%; Pred. No. 6.5e-159;  
Matches 558; Conservative 9; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57  
Db 1 mnkiyriiwnsalnawavseltrnhktrasatvktavlatllfatvgasanneegeedl 60

QY 58 YLEPVQRTFAVLFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116  
Db 61 yldpvqrtvavlivnsdkegtgekeveedsnwavyfdekgyvltareitlkagdnikikq 120

QY 117 NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEINGD 176  
Db 121 -----ngsnftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketagtn 174

QY 177 TTVHLNGIGSTLTDLTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNKIKVKGPGTTA 236  
Db 175 ttvhlngigstltdllntgattnvtndvtddekkraasvkdvl nagwnikgvkpgtta 234

QY 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGDK 296  
Db 235 sdnvdfvrydvtveflsadtktttvnveskdngkrtevkigaktsvikekdglvtgdk 294

QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGK 356  
Db 295 gengsstdegeglvtakevidavnkagwrmttttangtgqgadkfetvtsgtnvtfasgk 354

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSGKVISGNVSPSKG 416  
Db 355 gttatvskddqgnitvm ydvnvgdalnv nqlqns gwnlds kavagsgkv isgnvpskg 414

QY 417 KMDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 415 kmdetvinagnnieitrngknidiatsmt p qfssvslgagadap t lsvdgd -alnv gsk 473

QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQA 536  
Db 474 kdkpvr itnvapgvkegdvtnvaqlkgvaqnl nhr idnv dgnar agiaqaiataglvqa 533

QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 594  
Db 534 ylpgksmmai99gtyrgeagyaigyssisdggnwlikgtasgnsrghfgasasvgyqw 591

RESULT 11  
AAY23743  
ID AAY23743 standard; Protein; 599 AA.  
XX

AC AAY23743;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

OS Neisseria meningitidis.

PN WO9931132-A1.

XX

PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85795.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 114-115; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 599 AA;

Query Match 91.5%; Score 2762.5; DB 20; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.2e-157;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLYL 59  
Db 1 mnkiyriiwnsalnawavseltrnhktrasatvktavlatllfatvganatede 60

QY 60 EPVQRTAVLFRSDKEGTGEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116  
Db 61 epvrsalvqlfmidkeggenestgnigswlyydhntlhgatvtlkagdnlkikqntn 120

QY 117 -NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEING 175  
Db 121 kntnentndssftyslkkdltdltsveteklsfgangknvnitsdtkglnfaketagtn 180

QY 176 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNKIKVKGPGTT 235  
Db 181 dttvhlngigstltdllntgattnvtndvndvtddekkraasvkdvl nagwnikgvkpgtt 240

QY 236 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGKD 295  
Db 241 asdnvdfvhtydtveflsadtktttvnveskdngkrtevkigaktsvikekdglvtgk 300

QY 296 KGENDSSTDKEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFFASG 355  
Db 301 kgengsstdegeglvtakevidavnkagwrmttttangtgqgadkfetvtsgtntvf 360

QY 356 KGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSGKVISGNVSPSK 415  
Db 361 kgtatvskddqgnitv ydvnvgdalnv nqlqns gwnlds kavagsgkv isgnvpsk 420

QY 416 GKMDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475  
Db 421 gkmdetvinagnnieitrngknidiatsmt p qfssvslgagadap t lsvddk galnvgs 480

QY 476 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVGDNARAGIAQAIATAGLVQ 535  
Db 481 kdan kpvritnvapgvkegdvtnvaqlkgvaqnl nhr idnv dgnar agiaqaiataglvq 540

QY 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGRHFGASASVGYQW 594

Db 541 aylpgksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 599  
RESULT 12  
AAU06176  
ID AAU06176 standard; Protein; 599 AA.  
XX AC AAU06176;  
XX DT 24-OCT-2001 (first entry)  
XX DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.  
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX OS Neisseria meningitidis strain H38.  
XX FH Key Location/Qualifiers  
FT Region 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT Region 51..105  
FT /label= V1  
FT /note= "Variable region 1"  
FT Region 106..117  
FT /label= C2  
FT /note= "Conserved region 2"  
FT Region 118..131  
FT /label= V2  
FT /note= "Variable region 2"  
FT Region 132..195  
FT /label= C3  
FT /note= "Conserved region 3"  
FT Region 196..217  
FT /label= V3  
FT /note= "Variable region 3"  
FT Region 218..236  
FT /label= C4  
FT /note= "Conserved region 4"  
FT Region 237..243  
FT /label= V4  
FT /note= "Variable region 4"  
FT Region 244..599  
FT /label= C5  
FT /note= "Conserved region 5"  
XX WO200155182-A1.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-AU000069.  
XX PR 25-JAN-2000; 2000US-0177917.  
XX PA (UYQU ) UNIV QUEENSLAND.  
XX PI Peak IRA, Jennings MP;  
XX WPI; 2001-488774/53.  
XX N-PSDB; AAS09166.  
XX PT New Nhha surface antigen polypeptides and polynucleotides from  
XX PT Neisseria meningitidis, useful in producing vaccines for treating or  
XX PT preventing broad spectrum of Neisseria meningitidis -  
XX PS Claim 9; Fig 1; 9lpp; English.  
XX CC The present invention relates to the isolation of novel Neisseria  
XX CC meningitidis mutant polypeptides of the surface antigen Nhha  
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
XX CC characterised by deletions of non-conserved amino acids, particularly  
XX CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.  
XX SQ Sequence 599 AA;  
Query Match 91.5%; Score 2762.5; DB 22; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.2e-157;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWNALSNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLXL 59  
Db 1 mnkiyriiwnalsnawvavseltrnhtkrasatvktavlatllfatvqanatdedeeel 60  
QY 60 EPVORTAVVLSFRSDKEGTGEKTEDESDNWGVYFDKKGVLTAGTITLKAGDNLKIQ--- 116  
Db 61 epvvralsvlqfmidkegngenesnigwsiyydnhntlhgatvtlkgadnlkikqntn 120  
QY 117 -NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKTAETNG 175  
Db 121 kntnentndssftyslkkdltdltsveteklsfngangkvnitsdkglnfaketagtng 180  
QY 176 DTTVHLNGIGSTLDTLLNTGATTVNTDNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 235  
Db 181 dttvhlngigstltdllntgattndvndvtddekkraasvkdvlndnagwnkvgkpgtt 240  
QY 236 ASDNVDFVRTYDIVEFLSADTKTTTVNVESKDNKRTKTEVKIGAKTSVIKEKGLVTGKD 295  
Db 241 asdnvdfvhtydtveflsadtktttvnveskdngrtevkigaktsvikekdgklvtgk 300  
QY 296 KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT'TTANGQTGQADKFETVTSGTNTVFASG 355  
Db 301 kgengsstdegeglvtakevidavnkagwrmk'tttangqtgqadkfetvsgtnvtfasg 360  
QY 356 KGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 415  
Db 361 kgtatvskddqgnitvkdynvgdnlvnlqngsgwnldskavagssgkvisgnvspk 420  
QY 416 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS 475  
Db 421 gkmdetvniagnnieitrngknidiatsmtptgfssvslgagadaptsvddkgalnvgs 480  
QY 476 KDANKPVRITNVAPGVEGDTVNVQALKGVAQNLNHIDNVGNARAGIAQAIATAGLVQ 535  
Db 481 kdankpvritnvapgvegdvtnvaqlkgvaqnlndvndgnaragiaqaiataglvq 540  
QY 536 AYLPGKSMMAIGGGTYRGEAGYAICYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 541 aylpgksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 599  
RESULT 13  
AAU27202  
ID AAY27202 standard; Protein; 591 AA.  
XX AC AAY27202;  
XX DT 24-SEP-1999 (first entry)  
XX DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
XX KW bacterial infection; treatment.  
XX OS Neisseria meningitidis.

PN WO9936544-A2.  
XX 22-JUL-1999.  
PD  
XX  
XX  
PF 14-JAN-1999; 99WO-IB00103.  
XX  
XX  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
XX  
PI Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;  
XX  
DR WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
XX  
CC The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisserial  
CC bacteria, especially Neisseria meningitidis.  
XX  
XX  
SQ Sequence 591 AA;  
  
Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57  
Db 1 mnkiyriiwnlsalnawvvvseltrnhtrkrasatvktavlatllfatvqasanneeqedl 60  
  
QY 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116  
Db 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekgvitareitlkagdnlkikq 120  
  
QY 117 NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGD 176  
Db 121 -----ngtnftyslkkdltdltsvgtseklfsangknvnitsdtkglnfaketagtngd 174  
  
QY 177 TTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 ttvhlngigstltdtllntgattnvtndvtddekkraasvkdvlnagwnikgvkpgtta 234  
  
QY 237 SDNVDFVRTYDVEFLSADTKTTTVNVVESKDNGKRTVEKIGAKTSVIKEKDGKLVTKGDK 296  
Db 235 sdnvdfvrtydveflsadtktttnvveskdngkktevkigaktsvikekdgklvtgkdk 294  
  
QY 297 GENDSSTDGEGLVTAKEVIDAVNKAGWRMKTATTANGQTQADKFETVTSGTNVTFAFGK 356  
Db 295 gengsstdegeglvtakevidavnkagwrnktttangqtgqadkfetvtsgtntvfaskg 354  
  
QY 357 GTTATVSKDDGQGNITVMYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
Db 355 gttatvskddggnitvm ydvnvgdalnvnlqns gwnldskavagssgkvisgnvspkg 414  
  
QY 417 KMDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476  
Db 415 kmdetvinagnnieitrngknidiatmtptqfssvslgagadaptsvdgd-alnvgsk 473  
  
QY 477 DANKPVRITNVAPGVKEGDTVNVAQKGVQAQNLNNHIDVNDGNARAGIAQAIAATAGLVQA 536  
Db 474 kdkpvr itnvapgvkegdtvnvaqlkgvaqnl nnr idnv dgnar agiaqaiataglvqa 533

QY 537 YLPKGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594  
Db 534 ylpkgksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrgrhfgasasvgyqw 591  
  
RESULT 14  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
XX 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;  
  
Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57  
Db 1 mnkiyriiwnlsalnawvvvseltrnhtrkrasatvktavlatllfatvqasanneeqedl 60  
  
QY 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116  
Db 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekgvitareitlkagdnlkikq 120  
  
QY 117 NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGD 176  
Db 121 -----ngtnftyslkkdltdltsvgtseklfsangknvnitsdtkglnfaketagtngd 174  
  
QY 177 TTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 ttvhlngigstltdtllntgattnvtndvtddekkraasvkdvlnagwnikgvkpgtta 234

Db 175 ttvhlngigstltdllntgattnvtndnvtddekkraasvkdvltnagwnikgvkpgtta 234

QY 237 SDNVDFVRTYDVEFLSADTKTTVNVESKNGKRTVEKIGAKTSVIKEKDGLVTGDK 296

Db 235 sdhndfvrtYdtveflsadtktttvnnveskngkktvkvigaktsvikekgklvtgdk 294

QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTttTANGQTGQADKFETVTSNTNVTFASGK 356

Db 295 gengsstdegeglvtakevidavnkagwrmttttangqtgqadkfetvtsntnvtfasgk 354

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416

Db 355 gttatvskddqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskg 414

QY 417 KMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476

Db 415 kmdetvniagnnieitrngknidiatsmtppqfssvslgagadaptlsvdgd-alnvgsk 473

QY 477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHIDNVGNARAGIAQAIAATAGLVQA 536

Db 474 kdnkpvrItnvapgvkegdvtNvaqlkgvaqnlNnrIdnvdgnaragIaqaiaataglvqa 533

QY 537 YLPGKSMMaIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594

Db 534 ylpGksmmaIgggtyrgeagyaigYssisdgnwIIkgtasGnsrghfgasasvgyqW 591

RESULT 15

AAU06171

ID AAU06171 standard; Protein; 591 AA.

XX AC AAU06171;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain PMC21.

XX FH

PH Key Location/Qualifiers

FT Peptide 1..51 /label= Signal\_peptide

FT Region 1..50 /label= C1

FT Region /note= "Conserved region 1"

FT Region 51..108 /label= V1

FT Protein /note= "Variable region 1"

FT Protein 52..591 /label= Mature\_Nhha

FT Protein /note= "Predicted mature protein, specifically claimed in claim 12"

FT Region 109..120 /label= C2

FT Region /note= "Conserved region 2"

FT Region 121..124 /label= V2

FT Region /note= "Variable region 2"

FT Region 125..188 /label= C3

FT Region /note= "Conserved region 3"

FT Region 189..210 /label= V3

FT Region /note= "Variable region 3"

FT Region 211..229 /label= C4

FT Region /note= "Conserved region 4"

FT Region 230..236 /label= V4

FT Region /note= "Variable region 4"

FT Region 237..591

FT /label= C5

FT /note= "Conserved region 5"

XX WO200155182-A1.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU000069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI; 2001-488774/53.

DR N-PSDB; AAS09161.

XX New Nhha surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -

Claim 9; Fig 1; 91pp; English.

The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.

Sequence 591 AA;

Query Match 91.4%; Score 2758.5; DB 22; Length 591;

Best Local Similarity 92.3%; Pred. NO. 2e-157;

Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLFLFATVQASTTD---DDDL 57

Db 1 mnkiYriIwnsalnawvVseltrNhtkrasatvtavlatlLfafvqasanneeQeDl 60

QY 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKQ 116

Db 61 yldpvqrtvavliVnsdkegtgekeveensdwavyfnekgvltareitlkagDnlkikq 120

QY 117 NTNENTNASSETYSCLKKDLTDLTSVGTSEKLSFANSKNVNITSDTKGLNFAKKTAEtNGD 176

Db 121 -----ngtnftyslkkdltdltsvgteklSfsangknvItsdtkglnfaketaGtngD 174

QY 177 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTTA 236

Db 175 ttvhlngigstltdtlntgattnvtndnvtddkkraasvkdvlNagwnikgvkpgtta 234

QY 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIKEKDGLVTGDK 296

Db 235 sdndvfvrtYdtveflsadtktttvnnveskngkktvkvigaktsvikekgklvtgdk 294

QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTttTANGQTGQADKFETVTSNTNVTFASGK 356

Db 295 gengsstdegeglvtakevidavnkagwrmttttangqtgqadkfetvtsntnvtfasgk 354

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416

Db 355 gttatvskddqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskg 414



Search completed: September 5, 2002, 10:23:14  
Job time: 476 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:19:03 ; Search time 25.63 Seconds  
(without alignments)  
566.087 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASVGYQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3019	100.0	594	4	US-09-377-155-9
2	3019	100.0	594	4	US-09-669-974-9
3	2874	95.2	594	4	US-09-377-155-7
4	2874	95.2	594	4	US-09-669-974-7
5	2855	94.6	598	4	US-09-377-155-13
6	2855	94.6	598	4	US-09-669-974-13
7	2852	94.5	598	4	US-09-377-155-5
8	2852	94.5	598	4	US-09-669-974-5
9	2762.5	91.5	599	4	US-09-377-155-15
10	2762.5	91.5	599	4	US-09-669-974-15
11	2758.5	91.4	591	4	US-09-377-155-21
12	2758.5	91.4	591	4	US-09-669-974-21
13	2751	91.1	592	4	US-09-377-155-2
14	2751	91.1	592	4	US-09-669-974-2
15	2739.5	90.7	591	4	US-09-377-155-11
16	2739.5	90.7	591	4	US-09-669-974-11
17	2636	87.3	592	4	US-09-377-155-17
18	2636	87.3	592	4	US-09-669-974-17
19	2516.5	83.4	589	4	US-09-377-155-19
20	2516.5	83.4	589	4	US-09-669-974-19
21	1328.5	44.0	2353	4	US-09-377-155-33
22	1328.5	44.0	2353	4	US-08-913-942-4
23	1328.5	44.0	2353	4	US-09-669-974-33
24	1327.5	44.0	2354	4	US-09-268-347-47
25	1292.5	42.8	2411	4	US-09-268-347-36
26	1261	41.8	607	1	US-08-409-995-6
27	1261	41.8	607	3	US-08-685-467-6

28	1261	41.8	607	4	US-08-913-942-6	Sequence 6, Appli
29	1261	41.8	1912	1	US-08-409-995-4	Sequence 4, Appli
30	1261	41.8	1912	3	US-08-685-467-4	Sequence 4, Appli
31	1055	34.9	1094	4	US-09-268-347-32	Sequence 32, Appli
32	1030	34.1	1098	1	US-08-409-995-2	Sequence 2, Appli
33	1030	34.1	1098	3	US-08-685-467-2	Sequence 2, Appli
34	1030	34.1	1098	4	US-09-377-155-32	Sequence 32, Appli
35	1030	34.1	1098	4	US-08-913-942-2	Sequence 2, Appli
36	1030	34.1	1098	4	US-09-669-974-32	Sequence 32, Appli
37	1030	34.1	1098	4	US-09-268-347-44	Sequence 44, Appli
38	1016	33.7	658	1	US-08-409-995-5	Sequence 5, Appli
39	1016	33.7	658	3	US-08-685-467-5	Sequence 5, Appli
40	1016	33.7	658	4	US-08-913-942-5	Sequence 5, Appli
41	978.5	32.4	679	4	US-08-913-942-15	Sequence 15, Appli
42	978.5	32.4	679	4	US-09-268-347-26	Sequence 26, Appli
43	741	24.5	1004	4	US-09-268-347-30	Sequence 30, Appli
44	727	24.1	1002	4	US-09-268-347-24	Sequence 24, Appli
45	689	22.8	1104	4	US-09-268-347-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match	100.0%;	Score 3019;	DB 4;	Length 594;
Best Local Similarity	100.0%;	Pred. No. 1.5e-226;		
Matches 594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE	60	
Db	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE	60	
Qy	61	PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE	120	
Db	61	PVQRTAVVLSFRSDKEGTGEKTEVDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE	120	
Qy	121	NTNASSFTYSLKKDLTDLTSVGTEKLSFNSANSKNVNITSDTKGLNFAKKTAEKNGDITVH	180	
Db	121	NTNASSFTYSLKKDLTDLTSVGTEKLSFNSANSKNVNITSDTKGLNFAKKTAEKNGDITVH	180	
Qy	181	LNGIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNV	240	
Db	181	LNGIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNV	240	
Qy	241	DFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVIKEDGKLVTKDKGEND	300	
Db	241	DFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVIKEDGKLVTKDKGEND	300	
Qy	301	SSTDKGEGLVTAKEVIDAVNKAAGWRMKTTTTANGQTGQADKFETVTSGTNVTTFASGKGTTA	360	

Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVFASGKGTTA 360  
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
QY 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594

RESULT 2

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; TYPE: PRT  
; LENGTH: 594  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 100.0%; Score 3019; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.5e-226;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKEDVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKEDVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
QY 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEINGDTTVH 180  
Db 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEINGDTTVH 180  
QY 181 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240  
Db 181 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240  
QY 241 DFVRTYDTEFLSADTKTTTVNVEKDNKRGTEVKIGAKTSVKEKDGKLVTKDKKGEND 300  
Db 241 DFVRTYDTEFLSADTKTTTVNVEKDNKRGTEVKIGAKTSVKEKDGKLVTKDKKGEND 300  
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVFASGKGTTA 360

Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVFASGKGTTA 360  
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480  
QY 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHNDVGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594

RESULT 3

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 95.2%; Score 2874; DB 4; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.8e-215;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKEDVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKEDVSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEINGDTTVH 180  
Db 121 NTNASSFTYSLKKDLTDLTSVETEKLSEFGANGKNVNITSDTKGLNFAKKTAEINGDTTVH 180  
QY 181 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240  
Db 181 LNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV 240  
QY 241 DFVRTYDTEFLSADTKTTTVNVEKDNKRGTEVKIGAKTSVKEKDGKLVTKDKKGEND 300  
Db 241 DFVRTYDTEFLSADTKTTTVNVEKDNKRGTEVKIGAKTSVKEKDGKLVTKDKKGEND 300  
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVFASGKGTTA 360  
Db 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVFASGKGTTA 360  
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420

Db 361 TVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMD 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDTNK 480  
QY 481 PVRITNVAPGVKEGDTVNV AQLKGVAQNLNHNHIDNV DGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDTVNV AQLKGVAQNLNHNHIDNV DGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 594  
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 594

RESULT 4

US-09-669-974-7  
; Sequence 7, Application US/096669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 95.2%; Score 2874; DB 4; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.8e-215;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
  
QY 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
  
QY 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFANSKNVNITSDTKGLNFAKKTAEETNGD 180  
Db 121 NTNDSSTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGDPTVH 180  
  
QY 181 LNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTASDNV 240  
Db 181 LNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTASDNV 240  
  
QY 241 DFVRTYDVTVELSADTKTTTVNVESKDNGKRTVEVKIGAKTSVIKEKDKLVTKGKDENG 300  
Db 241 DFVRTYDVTVELSADTKTTTVNVESKDNGKRTVEVKIGAKTSVIKEKDKLVTKGKDENG 300  
  
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 360  
Db 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 360  
  
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMD 420

Db 361 TVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMD 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480  
Db 421 TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDTNK 480  
QY 481 PVRITNVAPGVKEGDTVNV AQLKGVAQNLNHNHIDNV DGNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRITNVAPGVKEGDTVNV AQLKGVAQNLNHNHIDNV DGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 594  
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 594

RESULT 5

US-09-377-155-13  
; Sequence 13, Application US/093771155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 94.6%; Score 2855; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 8.5e-214;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
  
QY 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
  
QY 121 NTNA----SFTYSLKKDLTDLTSVGTEKLSFANSKNVNITSDTKGLNFAKKTAEETNGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180  
  
QY 177 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 240  
  
QY 237 SDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNGKRTVEVKIGAKTSVIKEKDKLVTKGDK 296  
Db 241 SDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNGKRTVEVKIGAKTSVIKEKDKLVTKGDK 300  
  
QY 297 GENDSSTDKEGGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 356  
Db 301 DENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGN 360  
  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 420  
  
QY 417 KMDETVNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476



Db 421 KMDETVNIINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNVVAQLKGVQNLNNHIDNVGNARAGIAQAIAATAGLVQA 536  
Db 481 DANKPVRITNVAPGVKEGDTVNVVAQLKGVQNLNNRIDNVGNARAGIAQAIAATAGLAQA 540  
QY 537 YLPCKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPCKSMMAIGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW 598

RESULT 6  
US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 94.6%; Score 2855; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 8.5e-214;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKTEVEDSNWGVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
QY 121 NTNA----SSFTYSLKKDLTDLTSVGETEKLFSANSNKVNITSDTKGLNFAKKTAEANGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180  
QY 177 TTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 240  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGDK 296  
Db 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGKGK 300  
QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFFETVTSGTNVTFASGK 356  
Db 301 DENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFFETVTSGTNVTFASGN 360  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVNIINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476

Db 421 KMDETVNIINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNVVAQLKGVQNLNNHIDNVGNARAGIAQAIAATAGLVQA 536  
Db 481 DANKPVRITNVAPGVKEGDTVNVVAQLKGVQNLNNRIDNVGNARAGIAQAIAATAGLAQA 540  
QY 537 YLPCKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPCKSMMAIGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW 598

RESULT 7  
US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 94.5%; Score 2852; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.5e-213;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKTEVEDSNWGVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
QY 121 NTNA----SSFTYSLKKDLTDLTSVGETEKLFSANSNKVNITSDTKGLNFAKKTAEANGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180  
QY 177 TTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 240  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGDK 296  
Db 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGKGK 300  
QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFFETVTSGTNVTFASGK 356  
Db 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFFETVTSGTNVTFASGN 360  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVNIINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 421 KMDETVNIINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNVAPGVKEGDTVNVVAQLKGVQNLNNHIDNVGNARAGIAQAIAATAGLVQA 536

Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLAQA 540  
QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI I KGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTASVGYQW 598

RESULT 8  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 94.5%; Score 2852; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.5e-213;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
  
QY 1 MNKIYRIIWN S ALNAWAVSELTRNHTKRASATVATAV L L L F A T V Q A S T T D D D D L Y L E 60  
Db 1 MNKISRIIWN S ALNAWVVSELTRNHTKRASATVATAV L L L F A T V Q A N A T D D D D L Y L E 60  
  
QY 61 PVQRTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITL KAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTGEKTEVSDSNWAVFDEKRVLKAGAITL KAGDNLKIKQNTNE 120  
  
QY 121 NTNA----SSFTYSLKKDLTDLTSVGETEKL SFSANSKNVNITSDTKGLNFAKKTAE TNGD 176  
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180  
  
QY 177 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN IKGVPKGTTA 236  
Db 181 PTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN IKGVPKGTTA 240  
  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKDK 296  
Db 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKGK 300  
  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTQQADKFFETVTSGTNVTFASGK 356  
Db 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTQQADKFFETVTSGTKVTFASGN 360  
  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLD S KAVAGSSGKVISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLD S KAVAGSSGKVISGNVSPSKG 420  
  
QY 417 KMDET VNINAGNNIEITRNGKNIDIATSMTPOFSSVSLGAGADAPTLSVDDEGALNVGSK 476  
Db 421 KMDET VNINAGNNIEITRNGKNIDIATSMTPOFSSVSLGAGADAPTLSVDDEGALNVGSK 480  
  
QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLVQA 536  
Db 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLVQA 536

Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLAQA 540  
QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI I KGTASGNSRGHFGASASVGYQW 594  
Db 541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTASVGYQW 598  
  
RESULT 9  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 91.5%; Score 2762.5; DB 4; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.3e-206;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
  
QY 1 MNKIYRIIWN S ALNAWAVSELTRNHTKRASATVATAV L L L F A T V Q A S T T D - D D D L Y L 59  
Db 1 MNKIYRIIWN S ALNAWAVSELTRNHTKRASATVATAV L L L F A T V Q A N A T D E D E E E L 60  
  
QY 60 EPVQRTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITL KAGDNLKIKQ--- 116  
Db 61 EPVVRSAVLQFMIDKEGGENESTGNIGWSIYDHNHTLHGATVTL KAGDNLKIKQNTN 120  
  
QY 117 -NTNENTNASFTYSLKKDLTDLTSVGETEKL SFSANSKNVNITSDTKGLNFAKKTAE TNG 175  
Db 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 180  
  
QY 176 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN IKGVPKGT 235  
Db 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN IKGVPKGT 240  
  
QY 236 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKD 295  
Db 241 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKG 300  
  
QY 296 KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTQQADKFFETVTSGTNVTFASG 355  
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTQQADKFFETVTSGTNVTFASG 360  
  
QY 356 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLD S KAVAGSSGKVISGNVSPSK 415  
Db 361 KGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLD S KAVAGSSGKVISGNVSPSK 420  
  
QY 416 GKMDET VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS 475  
Db 421 GKMDET VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDK GALNVGS 480  
  
QY 476 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLVQ 535  
Db 481 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNV DGNARAGIAQAIAATAGLVQ 540  
  
QY 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI I KGTASGNSRGHFGASASVGYQW 594

Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 599  
RESULT 10  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 91.5%; Score 2762.5; DB 4; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.3e-206;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLYL 59  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDEDEEEL 60  
QY 60 EPVORTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116  
Db 61 EPVVSALVLQFMIDKEGNGENESTCNIGWSIYDNDHNTLHGATVTLKAGDNLKIKQNTN 120  
QY 117 -NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEENG 175  
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSEFGANGKNVNITSDTKGLNFAKETAGTNG 180  
QY 176 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTT 235  
Db 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTT 240  
QY 236 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDGKLVTKGD 295  
Db 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDGKLVTKG 300  
QY 296 KGENDSSTDKEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFFETVTSNTVTFASG 355  
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFFETVTSNTVTFASG 360  
QY 356 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK 415  
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK 420  
QY 416 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475  
Db 421 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480  
QY 476 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNHIDNVNAGNARAGIAQAIATAGLVQ 535  
Db 481 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNHIDNVNAGNARAGIAQAIATAGLVQ 540  
QY 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
|||||

Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 599  
RESULT 11  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 91.4%; Score 2758.5; DB 4; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2.6e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASANNEEQEEDL 60  
QY 58 YLEPVORTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116  
Db 61 YLDPVORTAVVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 117 NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAEENG 176  
Db 121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFSANGKNVNITSDTKGLNFAKETAGTNG 174  
QY 177 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTTA 236  
Db 175 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTTA 234  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDGKLVTKGDK 296  
Db 235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDGKLVTKGDK 294  
QY 297 GENDSSTDKEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFFETVTSNTVTFASGK 356  
Db 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFFETVTSNTVTFASGK 354  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 416  
Db 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 414  
QY 417 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 415 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALNVGSK 473  
QY 477 DANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNHIDNVNAGNARAGIAQAIATAGLVQA 536  
Db 474 KDNKPVRITNVAPGVKEGDTVNVQALKGVAQNLNHIDNVNAGNARAGIAQAIATAGLVQA 533  
QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594  
Db 534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591  
|||||



RESULT 12  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 91.4%; Score 2758.5; DB 4; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2.6e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

Qy	1	MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL	57
Db	1	MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL	60
Qy	58	YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ	116
Db	61	YLDPVQRTAVVLSFRSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ	120
Qy	117	NTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAE	176
Db	121	-----NCTNFTYSLKKDLTDLTSVGTSEKLSFSANGKNVNITSDTKGLNFAKETAG	174
Qy	177	TTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGT	236
Db	175	TTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGT	234
Qy	237	SDNVDFVRYDVTVEFLSADTKTTTNNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTG	296
Db	235	SDNVDFVRYDVTVEFLSADTKTTTNNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTG	294
Qy	297	GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKPFETVTSNTVTFAS	356
Db	295	GENGSSTDGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKPFETVTSNTVTFAS	354
Qy	357	GTTATVSKDDQGNITVMYDENVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	416
Db	355	GTTATVSKDDQGNITVMYDENVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	414
Qy	417	KMDETVMNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS	476
Db	415	KMDETVMNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGS	473
Qy	477	DANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNHIDNVGDNARAGIAQAIATAGLVQ	536
Db	474	KDNKPVRTNVAPGVKEGDTVNAQLKGAQNLLNNRIDNVGDNARAGIAQAIATAGLVQ	533
Qy	537	YLPKGSMAAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
Db	534	YLPKGSMAAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591

RESULT 13

US-09-377-155-2  
; Sequence 2, Application US/093777155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 91.1%; Score 2751; DB 4; Length 592;  
Best Local Similarity 92.0%; Pred. No. 1e-205;  
Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;

Qy	1	MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDD---DD	56
Db	1	MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNERPRKKD	60
Qy	57	YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK	115
Db	61	YLDPVQRTAVVLSFRSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK	120
Qy	116	QNTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNITSDTKGLNFAKKTAE	175
Db	121	Q-----NGTNFTYSLKKDLTDLTSVGTSEKLSFSANGKNVNITSDTKGLNFAKETAG	174
Qy	176	DTTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGT	235
Db	175	DTTVHLNGIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKGT	234
Qy	236	ASDNVDFVRYDVTVEFLSADTKTTTNNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTG	295
Db	235	ASDNVDFVRYDVTVEFLSADTKTTTNNVESKDNGKRTVEVKIGKTSVIKEKDGLVTG	294
Qy	296	KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKPFETVTSNTVTFAS	355
Db	295	KGENGSTDGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKPFETVTSNTVTFAS	354
Qy	356	KGTTATVSKDDQGNITVMYDENVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	415
Db	355	KGTTATVSKDDQGNITVMYDENVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	414
Qy	416	GKMDETVMNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS	475
Db	415	GKMDETVMNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGS	473
Qy	476	KDANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNHIDNVGDNARAGIAQAIATAGLVQ	535
Db	474	KDNKPVRTNVAPGVKEGDTVNAQLKGAQNLLNNRIDNVGDNARAGIAQAIATAGLVQ	533
Qy	536	AYLPKGSMAAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
Db	534	AYLPKGSMAAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	592

RESULT 14

US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 91.1%; Score 2751; DB 4; Length 592;  
Best Local Similarity 92.0%; Pred. No. 1e-205;  
Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDD---DD 56  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASANNERPRKKD 60  
QY 57 LYLPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK 115  
Db 61 LYLPVQRTAVVLSFRSDKEGTGEKEVEENSDWVYFNEKGVLTAREITLKAGDNLKIK 120  
QY 116 QNTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSAANSKNVNITSDTKGLNFAKKTAEITNG 175  
Db 121 Q-----NGTNFTYSLKKDLTDLTSVGTEKLSFSAANSKNVNITSDTKGLNFAKKTAEITNG 174  
QY 176 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTT 235  
Db 175 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTT 234  
QY 236 ASDNVDFVRTYDVEFLSADTKTTVNVESKDNKGRKTEVKIGAKTSVIKEKDGLVTGKD 295  
Db 235 ASDNVDFVRTYDVEFLSADTKTTVNVESKDNKGRKTEVKIGAKTSVIKEKDGLVTGKD 294  
QY 296 KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASG 355  
Db 295 KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASG 354  
QY 356 KGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKSKAVAGSSGKVISGNVSPSK 415  
Db 355 KGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKSKAVAGSSGKVISGNVSPSK 414  
QY 416 GKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475  
Db 415 GKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 473  
QY 476 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLLNHNIDNVDGNARAGIAQAIATAGLVQ 535  
Db 474 KDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNHNIDNVDGNARAGIAQAIATAGLVQ 533  
QY 536 AYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 534 AYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 592

RESULT 15  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 90.7%; Score 2739.5; DB 4; Length 591;  
Best Local Similarity 91.8%; Pred. No. 7.9e-205;  
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD--DDD 57  
Db 1 MNEILRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASANNEEQEEDL 60  
QY 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK 116  
Db 61 YLDPVLRVAVLVNSDKETGEKEVEENSDWVYFNEKGVLTAREITLKAGDNLKIK 120  
QY 117 NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSAANSKNVNITSDTKGLNFAKKTAEITNG 176  
Db 121 -----NGTNFTYSLKKDLTDLTSVGTEKLSFSAANSKNVNITSDTKGLNFAKKTAEITNG 174  
QY 177 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 TTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 234  
QY 237 SDNVDFVRTYDVEFLSADTKTTVNVESKDNKGRKTEVKIGAKTSVIKEKDGLVTGKD 296  
Db 235 SDNVDFVRTYDVEFLSADTKTTVNVESKDNKGRKTEVKIGAKTSVIKEKDGLVTGKD 294  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASG 356  
Db 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASG 354  
QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKSKAVAGSSGKVISGNVSPSK 416  
Db 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKSKAVAGSSGKVISGNVSPSK 414  
QY 417 KMDETVINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 476  
Db 415 KMDETVINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 473  
QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLLNHNIDNVDGNARAGIAQAIATAGLVQ 536  
Db 474 KDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNHNIDNVDGNARAGIAQAIATAGLVQ 533  
QY 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 534 YLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 591

Search completed: September 5, 2002, 10:23:46  
Job time: 283 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:20:33 ; Search time 34.15 Seconds  
(without alignments)  
1671.364 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWNALSALNAWAVS.....TASGNSRGHFGASASVGQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2758.5	91.4	591	2 G81133	adhesin NMB0992 [i
2	2533	83.9	592	2 A81888	probable surface f
3	620	20.5	298	2 I64138	adhesin homolog HI
4	398.5	13.2	2059	2 D82671	surface protein XF
5	384.5	12.7	1190	2 A82615	surface autotrans
6	375.5	12.4	1107	2 AC0976	probable adhesin Z
7	368.5	12.2	1588	2 A86036	probable adhesin E
8	368.5	12.2	1588	2 H91188	probable adhesin p
9	331.5	11.0	658	2 AH0110	hypothetical prote
10	244	8.1	1091	2 G64964	surface-exposed ou
11	239	7.9	1004	2 C82672	190K surface antig
12	224	7.4	2249	2 A41477	probable adhesin P
13	222	7.4	1018	2 H83135	high-molecular-wei
14	220	7.3	1536	2 A43855	adhesin AIDA-I pre
15	219	7.3	1286	2 S28634	hypothetical prote
16	219	7.3	4919	2 T31105	ydek protein - Esc
17	216.5	7.2	1325	2 AG2560	hypothetical prote
18	216	7.2	1487	2 D90803	AIDA-I adhesin-lik
19	214.5	7.1	949	2 D90803	probable adhesin Z
20	214.5	7.1	1005	2 H85611	probable autotrans
21	213	7.1	3705	2 AD0123	high-molecular-wei
22	211.5	7.0	1477	2 B43855	probable adhesin h
23	209.5	6.9	1910	2 AF0394	probable RTX famil
24	209	6.9	5188	2 B85547	hypothetical prote
25	209	6.9	5291	2 F90696	Aida-I adhesin-lik
26	208	6.9	1327	2 B90674	probable beta-barr
27	208	6.9	1349	2 E85524	sapB protein - Cam
28	205.5	6.8	936	2 I40711	hemolysin A precu
29	204.5	6.8	1577	2 A35140	

30	203.5	6.7	1343	2 D85724	hypothetical prote
31	203	6.7	1608	2 A28182	hemolysin A - Serr
32	203	6.7	4936	2 AH2515	hypothetical prote
33	201.5	6.7	1109	2 A56143	surface-array prot
34	200.5	6.6	1343	2 E90893	hypothetical prote
35	200	6.6	980	2 H90681	probable flagellin
36	200	6.6	980	2 D85532	probable structura
37	200	6.6	3013	2 AB0480	probable invasin Y
38	198	6.6	2020	2 C48399	ABC-type transport
39	197	6.5	2551	2 B98047	hypothetical prote
40	197	6.5	3029	2 S76109	hypothetical prote
41	195	6.5	1029	2 T30852	outer membrane pro
42	195	6.5	1417	2 A83080	hypothetical prote
43	194.5	6.4	4152	2 T31102	filamentous hemagg
44	194	6.4	920	2 I40614	surface array prot
45	194	6.4	2468	2 A83412	hypothetical prote

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C;Accession: G81133

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755

A;Accession: G81133

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-591 <TET>

A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB0992

Query Match 91.4%; Score 2758.5; DB 2; Length 591;

Best Local Similarity 92.3%; Pred. No. 1.5e-131;

Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNALSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57

Db 1 MNKIYRIIWNALSALNAWVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60

QY 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIQ 116

Db 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120

QY 117 NTNENTNASSFTYSLKKDLTDLTTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGD 176

Db 121 -----NGTNFTYSLKKDLTDLTTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGD 174

QY 177 TTVHLNGIGSTLTDTLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236

Db 175 TTVHLNGIGSTLTDTLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVKPGTTA 234

QY 237 SDNVDFVRTYDTVEFLSADTKTTIVNVESKDNKGRTEVKIGAKTSVIKEKDGLVTGDK 296

Db 235 SDNVDFVRTYDTVEFLSADTKTTIVNVESKDNKGRTEVKIGAKTSVIKEKDGLVTGDK 294

QY 297 GENSSSTDKGEGGLVTAKEVIDAVNKAGWRMKT---TANGQTGQADKFETVTSNTVTFASGK 356

Db 295 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKT---TANGQTGQADKFETVTSNTVTFASGK 354

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLONGWNLDSKAVAGSSGKVISGNVSPSKG 416



||||| 355 GTTATVSKDDQGNITVMYDVNVGDALNVQLQNSGWNLDISKAVAGSSGKVISGNVSPSKG 414

QY 417 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476

Db 415 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVGD-ALNVGSK 473

QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVNVDGNARAGIAQAIAATAGLVQA 536

Db 474 KDNKPVRTNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVNVDGNARAGIAQAIAATAGLVQA 533

QY 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

Db 534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 2

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C;Accession: A81888

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556

A;Accession: A81888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-592 <PAR>

A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989

A;Experimental source: serogroup A, strain 22491

C;Genetics:

A;Gene: NMA1200

Query Match 83.9%; Score 2533; DB 2; Length 592;

Best Local Similarity 86.4%; Pred. No. 3.2e-120;

Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLLFATVQASTTD-DDDLYL 59

Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLLFATVQANATDEDEEEL 60

QY 60 EPVQRTAVVLSFRSDKEGTGEKE-----VTEDSNWGVYFDKKGVLFRAGTITLKAGDNLKI 114

Db 61 ESVQR-SVVGSIQASMEGSGELETTISLWNTDS-----KEFVDPIVVVTLKAGDNLKI 112

QY 115 KONTNENTNASSFTYSLKKDLTDLTSVGTGTEKLSFSANSKNVNITSDTKGLNFAKKTAEIN 174

Db 113 KONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTN 172

QY 175 GDTTVHLNGIGSTLTDLTFLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVPKT 234

Db 173 GDTTVHLNGIGSTLTDLTAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVTGS 230

QY 235 TA--SDNVDFVRTYDVEFLSADTKTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLV 292

Db 231 TTGQSENVDFVRTYDVEFLSADTKTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLV 290

QY 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSGTNVT 352

Db 291 GKKGGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSGTNVT 350

QY 353 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVS 412

Db 351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVS 410

QY 413 PSKGKMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALN 472

Db 411 PSKGKMDETVNIAGNNIEISRNGKNIDIASMAPQFSSVSLGAGADAPTLSDVDEGALN 470

QY 473 VGSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVNVDGNARAGIAQAIAATAG 532

Db 471 VGSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVNVDGNARAGIAQAIAATAG 530

QY 533 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGY 592

Db 531 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGY 590

QY 593 QW 594

Db 591 QW 592

RESULT 3

I64138

adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997

C;Accession: I64138

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630

A;Accession: I64138

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-298 <TIGR>

A;Cross-references: GB:U32846; GB:L42023; NID:gl574588; PID:gl574589; TIGR:HI1732

Query Match 20.5%; Score 620; DB 2; Length 298;

Best Local Similarity 46.6%; Pred. No. 2e-24;

Matches 145; Conservative 41; Mismatches 91; Indels 34; Gaps 7;

QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLATLLLFATVQASTTDDDDLXLE 60

Db 1 MNKIFKVIWNVVTQTWVVVSELTRAHTRKTSATVATAVLATVLSATVQA----- 49

QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLFRAGT-TITLKAGDNLKIKQNTN 119

Db 50 -INDAGTFVKVQSTEDDIEDSAATKDDN-----KNQALKAGDTTLTKAGKNLAKL--- 99

QY 120 ENTNASSFTYSLKKDLTDLTSVGTGTEKLSFSAN-----SNKVNITSDTKGLNFAKKTAE 172

Db 100 -DQGGKSVTFALAKDLVDKTKAVSDTLTIGGNTPAAGATPKVSITSTADGLKLAK---G 155

QY 173 TNGDTTVHLNGIGSTLTDLTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKGVPK 232

Db 156 TNGDTAVHLNGLASTLPDVTNTGASISVT-FSPSDIEKTRAATIKDVLNAGWNIKGAKV 214

QY 233 GTTASDNVDVVRTYDVEFLSADTKTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLV 292

Db 215 AGGNTENVDLVAGYDNVEFITGDKNTLDVVLTAKEGKTEVKFTPTPKTSVIKDNNGKLLT 274

QY 293 GKDKGENDSST 303

Db 275 GKQLKDANTGT 285

RESULT 4

D82671

surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C;Accession: D82671

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below





Db 1003 F-----VKVNSLNN-----SATPIAAGVDATAIGVGATASGADSI 1037

QY 461 -----PTLSVDDEGAL-----NVGSKDANKPVRITNVAPGVKEGDTVNVQAOLK 503

Db 1038 AMGNKASASADNAVAIGNHSVADRANTVSVGSAGSER--QVTINVAAGTADTDAVNVSQLN 1095

QY 504 GVAQNLNHHIDVNDGNAR----AGTAAAIATAGLVQAAYLPKGSMMMAIGGGTYRGEAGYAI 559

Db 1096 QGLITAKQYTDGVVGSRLRDTDGGVAAAIAATANLPQAYIPGRGMTSVGVSSYRGQSAIAV 1155

QY 560 GYSSLSDDGNNWIIKGTASGNSRGHFGASASVGYQW 594

Db 1156 GVSSVSESGRWVFKFSGSANTRSQVGIGAGVGYQW 1190

RESULT 6

AC0976

probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar typhi

C:Species: Salmonella enterica subsp. enterica serovar typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0976

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

C:Genetics:

A:Gene: sapB

Query Match 12.4%; Score 375.5; DB 2; Length 1107;

Best Local Similarity 21.7%; Pred. No. 2.1e-11;

Matches 185; Conservative 105; Mismatches 262; Indels 299; Gaps 33;

QY 27 TKRASATVATAVATLLFATVQASTD-----DDLY---LEPVQRTAVVLSFRSDKEGTGE 80

Db 273 TFSASRNGSASKITNLAAGTLAADSTDAVNGSOLYETNQKVDQNTSAIDINTSITNLSS 332

QY 81 KEVTEDSNWGVYFDKKGVLTAGTIT-LKAGD-----NLKIKQNT----- 118

Db 333 DNLWNETNSFSASHGSSTNKITNVAAGSESTDAVNGSOLFETNEKVQDQNTTIDIA 392

QY 119 -----NENTNASSFTYSLKKDLTDLTSVGTGKLT-SFSAN--SNKVNITSDT 161

Db 393 ANTTNITQNSTAIENLNTSVSDINTSI-TGLTDNALLWDEDTGAFSANHGGSTSKITNVA 451

QY 162 KGLNPAKKTAEONG-----DTTVHLNGIGSTLTDTLNTGATTNVTNDNVTDDEKKRAASV 217

Db 452 AGALSEDSTDAVNGSOLYETNQKVDQNTSAIAD--INT-SITNLGTDALSWDDEGAFSA 508

QY 218 KDVLNAGWNIKGVPKPGTTASDNVDFV---RTYDT-----VEFLSADTKTTTVN-- 262

Db 509 SHGTSQTNKITNVAAGEIASDSTDAVNGSOLYETNMLISQYNESISQLAGDTSITYTEN 568

QY 263 -----VESKDNQGRTEVKIGAKTSVIKEKDKLVTKGDK----- 306

Db 569 GTGVKYIRTNDNGLEGQ-----DAYATGNATAVAGYDAVASGAGACLAGQNSSSSIEG 621

QY 307 -----EGLV-----TAKEVIDAVNKA-----GWRMKTITAN 332

Db 622 STALGSGSTSNRAITTGIRETSATSDGVVIGYNTDRELLGALSLGTDGESYRQITNVAD 681

QY 333 QQTGQ-----ADKFETVTSQTNVTTFASGKGHTA---TVSKDDQG-- 368

Db 682 GSEAQDAVTVRQLQNALGAVTTTPTKYYHANSTEEDSLAVGTDSLAMGAKTIIVNADAGIG 741

QY 369 ---NITVMYDVNVGDALNVN-----QLQNSGWNLDSEK----- 397

Db 742 IGLNLTVMADAINGIAIGSNARANHANSHANSIAMNGSQTTRGAQTDYFAYNMDTPQNSVGEF 801

QY 398 AVAGSSGKVIISGNVSPSKGKMDETVNIAG---NNIEITRNKNI----- 439

Db 802 SVGSEGGQROITNVAAGSADTDA---VNVGQLKVTDAQVSRNTQSITNLNTQVSNLDRV 858

QY 440 -----DIATSMTPQF-----SSVSLGAGADAP-----TLSVDDE 468

Db 859 TNIENGIGDIVTTGSTKYFKTNTDCADANAQAQADSVAIGSGSIAAAENSVALGTNSVADE 918

QY 469 -GALNVGSKDANKPVRITNVAPGVKEGDTVNVQAOLK----- 503

Db 919 ANTVSVGSSTQOR--RITNVAAGVNTDVAVNVAQLKASEAGSVRYETNADGSVNVSVNL 976

QY 504 -----GVAQ-----NLNNHIDNVDCGNARAG 523

Db 977 GDGSGGTTTRIGNVSAAVNDTDVAVYAQLKRVEEANTYTDQKMGEMNSKIKGIENKMSGG 1036

QY 524 IAQAIATAGLVQAAYLPKGSMMMAIGGGTYRGEAGYAI GYSSISDGGNWIICKGTASGNSRGH 583

Db 1037 IASAMAMAGLPQAYAPGANMTSIAGGTENGESAVAIGVSMVSESGGVYKLGQTSNSQGD 1096

QY 584 FGASASVGYQW 594

Db 1097 YSAAIGAGFQW 1107

RESULT 7

A86036

probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: A86036

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A86036

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1588 <STO>

A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; DWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5029

Query Match 12.2%; Score 368.5; DB 2; Length 1588;

Best Local Similarity 23.0%; Pred. No. 7.4e-11;

Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;

QY 7 IIW-----NSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60

Db 880 LLWDADAGENGAFSA-----AHGKDKTASVITNV-ANGAISAASSDAINGSQLY-- 927

QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITL-----KAGDNLKI 114

Db 928 -----TTNKYIADALG-GDAEVNAD-----GTITAPTYTIANAEYNNVGDALDA 970

QY 115 KQNT---NENTNASSFTY-----SLKKDLTDL---TSVGTGKLSFSA 150

Db 971 LDDNALLWDETANGAGAYNASHDCKASIIITNVANGSISEDSTDAVNGSQLNATNMIEQ 1030

QY 151 NSKNVN-----ITSDTKGLNPAKKTAEETNGTPTVHLNGI----- 184

Db 1031 NTQIINQLAGNTDATYIQENGAGINVTNRDNDGLAFNDASAQGVGATAIGYNSVAKGDSS 1090

QY 185 -----GSTLTDTLNTGA-TTNVTNDNV-----TDDEKKRAASVKD 219

Db 1091 VAIGQSYSDVDTGIALGSSSVSSRRIAAGSRDTSITENGVVIGYDTTDCGELLGALSIGD 1150  
QY 220 -----VLNAGWNIKGVPKPGTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGK --- 270  
Db 1151 DGKYRQIIN-----VADGSEAHDAVT-VRQLONAIGAVATPTPKYFHANSTEEDSLAV 1202  
QY 271 -RTEVKIGAKTSVKEK-----DGKLVTKDKKGEND-----SSTDKEGGLVTAKE 314  
Db 1203 GTDSLAMGAKTIIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVNSIAIGNGSTTTRG 1262  
QY 315 V-----IDAVNKAGWRMKTTTANGQ-----TGQADKFETVTSGTNVTFFASGKGTT 359  
Db 1263 AQTNYTAYNMDAPQNSVGEFSVGSADGQRQITNVAAGSAD-----TDAVNV--GQLKVTD 1315  
QY 360 ATVSKDDQGNITVM-----YDVNVGDAL-----NVNQLQNSGWNLDS 396  
Db 1316 AQSQNTQ-SITNLDNRVTNLDNRVTNIENGIGDIVTTGSTKYFKTNTDGDVDSAAQKDS 1374  
QY 397 KAVAGSSGKVISGNVSPSKGKM---DETVNINAGNNIEITRN---GKNIDIATSMTPQFS 450  
Db 1375 VAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNQRRTITNVAAGKNATDAVNVAQLKS 1434  
QY 451 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDTVNVVAQLKGVAQ --- 507  
Db 1435 SEAGGVRYDTKADGSIDYSNITLGGNGG-TTRISNVSAGVNNNDVVNYAQLKQSVQETK 1493  
QY 508 -----NLNNHIDNVGNARAGIAQAIAATAGLVQAYLPKGSMMAIGGTYRGEAGYAI 559  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIGGTYNGESAVAL 1553  
QY 560 GYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
Db 1554 GVSMTVSANGRWVYKLOGSTNSQGEYSAAALGAGIQW 1588  
RESULT 8  
H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C;Accession: H91188  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91188  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1588 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g133633955; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs4480

Query Match 12.2%; Score 368.5; DB 2; Length 1588;  
Best Local Similarity 23.0%; Pred.No. 7.4e-11;  
Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;  
QY 7 IIW-----NSALNAWVAVSELTRNHTKRASATVATFAVLATLLFATVQASTTDDDDLYLE 60  
Db 880 LLWDADAGENGAFSA-----AHGKDKTASVITNV-ANGAISAASSDAINGSQLY-- 927  
QY 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNWGVYFDKKGVLTAGTITL-----KAGDNLKI 114  
Db 928 -----TTNKYIADALG-GDAEVNAD-----GTITAPTYYTIANAEYNNVGDALDA 970  
QY 115 KQNT-----NENTNASSFTY-----SLKKDLTDL---TSVGT EKLSFSA 150  
Db 971 LDDNALLWDETANGGAGAYNASHDGKASIIITNVANGSISEDSTDAVNGSQLNATNMWIEQ 1030  
QY 151 NSNKVN-----ITS DTKGLNFAKKTAE TNGD TTVHLNGI----- 184

Db 1031 NTQIINQLAGNTDAFYIQENGAGINYVRTNDDGLAFNDASAQGVGATAIGYNSVAKGDSS 1090  
QY 185 -----GSTLTDTLLNTGA-TTNTVNDNV-----TDDEKKRAASVKD 219  
Db 1091 VAIGQSYSDVDTGIALGSSSVSSRRIAAGSRDTSITENGVVIGYDTTDCGELLGALSIGD 1150  
QY 220 -----VLNAGWNIKGVPKPGTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGK --- 270  
Db 1151 DGKYRQIIN-----VADGSEAHDAVT-VRQLONAIGAVATPTPKYFHANSTEEDSLAV 1202  
QY 271 -RTEVKIGAKTSVKEK-----DGKLVTKDKKGEND-----SSTDKEGGLVTAKE 314  
Db 1203 GTDSLAMGAKTIIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVNSIAIGNGSTTTRG 1262  
QY 315 V-----IDAVNKAGWRMKTTTANGQ-----TGQADKFETVTSGTNVTFFASGKGTT 359  
Db 1263 AQTNYTAYNMDAPQNSVGEFSVGSADGQRQITNVAAGSAD-----TDAVNV--GQLKVTD 1315  
QY 360 ATVSKDDQGNITVM-----YDVNVGDAL-----NVNQLQNSGWNLDS 396  
Db 1316 AQSQNTQ-SITNLDNRVTNLDNRVTNIENGIGDIVTTGSTKYFKTNTDGDVDSAAQKDS 1374  
QY 397 KAVAGSSGKVISGNVSPSKGKM---DETVNINAGNNIEITRN---GKNIDIATSMTPQFS 450  
Db 1375 VAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNQRRTITNVAAGKNATDAVNVAQLKS 1434  
QY 451 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDTVNVVAQLKGVAQ --- 507  
Db 1435 SEAGGVRYDTKADGSIDYSNITLGGNGG-TTRISNVSAGVNNNDVVNYAQLKQSVQETK 1493  
QY 508 -----NLNNHIDNVGNARAGIAQAIAATAGLVQAYLPKGSMMAIGGTYRGEAGYAI 559  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIGGTYNGESAVAL 1553  
QY 560 GYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
Db 1554 GVSMTVSANGRWVYKLOGSTNSQGEYSAAALGAGIQW 1588  
RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C;Accession: AH0110  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB00001; MUID:21470413; PMID:11586360  
A;Accession: AH0110  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-658 <KUR>  
A;Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C;Genetics:  
A;Gene: YPO0902

Query Match 11.0%; Score 331.5; DB 2; Length 658;  
Best Local Similarity 25.0%; Pred. No. 1.7e-09;  
Matches 132; Conservative 73; Mismatches 209; Indels 113; Gaps 21;  
QY 99 LTAGTITLKAGDNLIKONTNENTNASSFTYSLKKDLTDLT SVGTEKLSFSANSKNVNIT 158  
Db 214 LGAGAVTSQA--NSIALGAASINTVGAQSSYSAYALTAPQASVGLGIGTALGNRKIT-- 269  
QY 159 SDTKGLNFAKKTAE TNGD TTVHLNGIGSTLTDTLLNTGATTNVTN--DNVTDDEKKRAAS 216  
Db 270 -----GVAAGSASSDAVNVAQLTAVGDQVQON-----TANITSLGRVTTIE----GS 313



QY 217 VKDVLNAGWNIKGVKPGTTASDNVDEVRTYDTVEFLSADTKTTTVNVESKDNGKRT - - - 272  
Db 314 MASIANGG-GVKYFHANSTQPSV - - - - - ASGTNSVAIGPASLASGNAALASG 360  
QY 273 --EVKIGAKTSVKEKDKLVTKGDKGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTIT 330  
Db 361 AGAVAIG--DGAASADGSAIGQSGDN - - - - - GRGV--ENVIGKYSNA - - - - -SNT 404  
QY 331 ANGQTQADKFETVTSNTVFASGKGTATATVSKDDQGNITVMYDVNVGDALNVQLQNS 390  
Db 405 SSG - - - - -TVSVGNTAT - - - - -GETRTVSNVADG - - - - -LQATDAVNLRLQD - 442  
QY 391 GWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNINAGNNI-EITRNGKNIDI--ATSMTP 447  
Db 443 - - - - -IAASIVVVENNVGSLQNGTDGMFQVNNSSGLAKPSATGANSATGGAGSVAS 493  
QY 448 QFSSVSLGAGADAPTLS - - - - -VDDEGALNVGSKDANKPVRITNVAPGVKEGDVTN 498  
Db 494 GNNSTAFGSGAKATAANSAAALGANSVADRANSVSGSVGNER--QITNVAPATQGTDAVN 551  
QY 499 VAQLKGVAQNLNHIDNVGNAR - - - - -AGIAQAIATAGLVQAYLPGKSMMAIG 547  
Db 552 FDQLKSISQNTNAYTNQRYSELKQDLRKQNSVLSAGIASAMSLTQPYTSGSSMTTIG 611  
QY 548 GGTyrGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGyQW 594  
Db 612 AASYRQGSALSLSGVSSISDSGRWVSKLQASSNTQGDGFGIGVGyQW 658  
RESULT 10  
G64964  
hypoetical protein b2000 - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
C:Accession: G64964  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: G64964  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1091 <BLAT>  
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g1788309;  
A:Experimental source: strain K-12, substrain MG1655  
C:Keywords: nucleotide binding; p-loop  
F:683-690/Region: nucleotide-binding motif A (p-loop)  
Query Match 8.1%; Score 244; DB 2; Length 1091;  
Best Local Similarity 22.6%; Pred. No. 8.3e-05;  
Matches 141; Conservative 64; Mismatches 215; Indels 204; Gaps 28;  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRSATVATAVLATLLEATVQASTTDDDLYLE 60  
Db 57 LNTCYRLVWNHMTGAFVVA SELARARGKRGVAVALSAAVTSPLVLA - - - - -DIVVH 110  
QY 61 PVQRTAVVLSFRSDKEGTGEKTEVETEDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKQNTNE 120  
Db 111 P - - - - -GE - - - - -TVNGGTLANHDNQIVFGTTNG 134  
QY 121 NTNASSFTYSLKKDLTDLTSVGTGKLSFSANSKNVITSDTKGLNFAKKTAEINGDITVH 180  
Db 135 MTISTGLEXPDPNE - - - - -ANTGGQVVDGGTANKTIVTSG--GLQRVNPGGSVS-DTVIS 187  
QY 181 LNGTGSTL - - - - -TDTLLNTG - - - - -ATTNVTNDNVTDDEKRAASVKDVLNAGWNI 227  
Db 188 AGG-GQSLOGRAVNTTLNGGEQWHEGAIAATGTVINDK - - - - -GWQV 228  
QY 228 KGVKPGTTASDNVDEVRT - - - - -YDTVEFLSADTKTTTVNVESKDNGKRTVEKIG 277  
Db 229 --VKPGTVATDV--VNTGAEGGPDANGDTGQVVRGDAVRTTN - - - - -KNGRQIVRAEG 280

QY 278 -AKTSVIKEKDKLVTKGDKGENDSSTDKGEGLV - - - - -TAKEVIDAVNKAGWRM - - - - - 326  
Db 281 TANITVVYAGGDQTVHGH - - - - -ALDITLNGGYQYVHNGGTASDTV--VNSDGMQIVKNGGV 335  
QY 327 -KTTTANGOTGQADKPFETVTSNTVFASG - - - - -KGTATATVSKDDQGNITVMYDVNVGDA 381  
Db 336 AGNTTVN-QKGR - - - - -QVDAGGTATNVTLKQGGALVTSTAATVT - - - - - 375  
QY 382 LNVNQLONGSWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNINAGNNIEITRNGKNIDI 441  
Db 376 -GINRL - - - - -GAFSVVEGKADNV - - - - -LENGGRLDV 403  
QY 442 ATSMTPQFSSVSLGA - - - - -GADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGD 495  
Db 404 LTGHTATNTRVDDGGTLDVRNGGTATTVSMGNGGVLLADSGAAVSGTRSDGKAFSIGGGQ 463  
QY 496 VTNVAQLKGVAQNLNHIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEA 555  
Db 464 ADALMLEKSGSFTLN - - - - -AGDTATDTT - - - - -VNGGLFTARG 497  
QY 556 GYAIGYSSISDGGNWIITKGTASGN 579  
Db 498 GTLAGTTTLNNGAILTLGSKTVNN 521  
RESULT 11  
C82672  
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: C82672  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82672  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carr  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1516  
Query Match 7.9%; Score 239; DB 2; Length 1004;  
Best Local Similarity 22.0%; Pred. No. 0.00013;  
Matches 158; Conservative 96; Mismatches 293; Indels 172; Gaps 33;  
QY 2 NKIYRIIWNALNAWVAVSELTRN - - - - -HTKRASATVATAVLATLLEATVQASTT 52  
Db 4 NQIYRKFVNLGLGSWSVASHMTNDGCCSDVLRHSGVVRNRSVLVLAIGLALTSVTHAQSVK 63  
QY 53 DDDLLYLEPVQRTA - - - - -VVLFSRSDKEGTGEKTEVETEDS - - - - -NWGV - - - - - 91  
Db 64 - - - - -SPAMVTASKVMVAHVDSQVNRRTADRIPTGDGSELMTMALDWMKFFPFGNNSIA 116



Qy	92	--YFKKGVLTAGTITLKAGDNLIKQNTN-----ENTNASSEFY-----SLKKDLTD	137
Db	117	IGYFKAFAPNA---IALGYNSSVTQSANNGVALGSNSTVSGVNSVALGAGSMASELNV	172
Qy	138	LTSVCTEKLFSANSNKVNITSDTKGLNFAKKTAEETNGDTTVHLNGIGISTLTDTLNTGA	197
Db	173	ISVGGDGVTPAVRRIVNV-GDGI GNDAVNKSQLDG-VTASVNDVAASKYTIAL---	226
Qy	198	TTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTASDNVDFVRTYDVEEFLSADT-	256
Db	227	TNQVTGSSVA-----SASKESTAIGSGAQAVADNTVAFGGRAIANAVG-ASALGFDSH	279
Qy	257	---KTTTVNVESKD-----NGKRTEVKIGAKTSVIKEKDGLVTGKD--	295
Db	280	AKGINSTTVGTQSVSLQGQVSLGLYNSFVGESEFNGLALGSNSLVLLQGVDSVALGSGSM	339
Qy	296	-KGENSDSTDKGEGL--VTAKEVI-----DAVNKAGWRMKTTTTANGOTQOADKFET	343
Db	340	ASEPNVYVSGSGDGLRGPVARRIVNVGDGIGNNDVAVNKSQLDGVTAASVNDVVASVKNIAG	399
Qy	344	V--TSCTNVTFASGKGTTAT-VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLD----	395
Db	400	AIQITCSGVASVSGQDSTAACASAAQAGDSSIA----LGARSRANAIGSSALGVGDHALG	455
Qy	396	--SKAVAGSSGKVISGVNVSPSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVS	453
Db	456	ANSTALGGQSTAISEGGTSLG---YNSFVGQSATNGIALGSN-----AIVSGVNSVA	504
Qy	454	LGAGADAPTLSDVDEGALNVGSKD-ANKPV--RITNVAPGVKEGDVTNVAQLKGVAQNLN	510
Db	505	LGAGSVASELNV-----ISVGGDGVGTGPVARRIVNVGDGIGNNDVAVNKSQLDGVTAASN	559
Qy	511	N---HIDNVDGNA---AGIAQAI---ATAGLVQAYLPKSMMAIG-----	547
Db	560	DVAASVKKIVGTIQITGSGVASAIGKDDSTATGASAAQAVGDSVALGTRATANAIGSSVLG	619
Qy	548	-----GGTYRGEAGYATGYSSISDGGNWIIK-----GTASGNSRGHFGA-SASVGY	592
Db	620	VDSRARGINSTALGRQSNALGDGVSVLGSFNFSFVRQSGEHGVALGTDAGVSGKDSIALGY	678

```

RESULT 12
A41477
190K surface antigen precursor - Rickettsia rickettsii
C:Species: Rickettsia rickettsii
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999
C:Accession: A41477
R:Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.
Infect. Immun. 58, 2760-2769, 1990
A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly
A:Reference number: A41477; MUID:90354033
A:Accession: A41477
A:Molecule type: DNA
A:Residues: 1-2249 <AND>
A:Cross-references: GB:M31227; NID:g152465; PIDN:AAA26380.1; PID:g152466
A:Note: the authors translated the codon GAT for residue 430 as Gly, and C
C:Keywords: surface antigen; tandem repeat
F:1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>

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Query Match 7.4%; Score 224; DB 2; Length 2249;  
Best Local Similarity 24.2%; Pred. No. 0.0021;  
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

QY	13	LNAWAVSELTRN--HTKRASATVATAVLATLLFATVQASTTDDDDL-----YLEPVQRT	65
Dd	640	LNLGALSQVTGDIGNTNSLATISVGAGTATLGGAVIKATTKITNAVSAVKFTNPVVVT	699
QY	66	AVVLSFRSDKEG---TGEKEVTEDSNWGVYFDKKGVLT---AGTITLKAGDNLKIKQN	117
Dd	700	GAI DSTGNANNGIVTFGTNSTVTGDIG-----NTNALATVNVVGAGTATL---GGAVIKAT	751
QY	118	TNENTNASSFTYSLKKOLDTLDSVGTKEKLSFSANSNKVNITSDTKGLNFAKKTAE TNGDT	177

Db	752	TTKLTNAASVL-----TLTNANAVLTGAIDNTTGGDNVGV-----LNLNGALSQVTDG- 799
Qy	178	TVHLNGIGSTLTDTLNTGATTNVTDNV---TDDEKKRAASVKDVLNAGWNIKGVKPGT 234
Db	800	-----IGNTNSLATISVGAGTATLGGAVIKATTKLTNAASVLTLTNANAVLTGAVDNT 853
Qy	235	TASDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTEVKIGAKT-----SVIKEKDCK 289
Db	854	TGGDNVGVNLNGALSQVTDIGNT-----NSLAT-ISVGAGTATLGGAVIKATTKK 904
Qy	290	L-----VTGKDKGENDSSTDCKEGL 309
Db	905	LTNAASVLTLTNANAVLTGAIDNTTGGDNVGVNLNGALSQVTVG-DIGNTNSLATISVGA 963
Qy	310	VTA-----KEVIDAVNKAGWRMKTTTANGQTGOADKFEVTVTSNTVFASGKGTTATV 362
Db	964	GTATLGGAVIKATTKLTDAASAVKFTNPVVVTGAIDNTGNANNGI-VTFTGNSTVTVGNV 1022
Qy	363	SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVVISGNVSPSKGMDETV 422
Db	1023	-----GNTNALATVNVGAGL--LQVQGGVVVKANTINLTDNASAVFTNPVVVTGAIDNTG 1075
Qy	423	NINAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGAG-----ADAPTLSDVDEG 469
Db	1076	NANNGIVTFTGNSTVTVGNVGN-----TNALATVNVGAGLLQVQGGVVVKANTINLTDNA 1128
Qy	470	ALNVGSKDANKPVRITNVAPGVKEGDVTNVVQLKGVAONLNHNHIDNVVDGNARA-----GIA 525
Db	1129	S-----AVTFEN-PPVVVTGAIDNTG-----NANNGIVTFTGNSTVTVTDIGNT 1169
Qy	526	QAIAT-----AGL-VQAYLPKGSMMA-----IGGGTYRGEAGYAIGY--- 561
Db	1170	NALATVNVGAGITLQA--GGSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYFK 1220
Qy	562	SSISDGGNWIK-----GTASGNSRGH---FGASASVG 591
Db	1221	GAIANGNNAILNVNTKLLTASHLTIGTVAEINIGAGNLFITDASVG 1266

RESULT  
H83135

probable adhesin PA4082 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83135  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337  
A:Accession: H83135  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1018 <STO>  
A:Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AAG07469.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4082

Query Match 7.4%; Score 222; DB 2; Length 1018;  
Best Local Similarity 22.5%; Pred. NO. 0.00097;  
Matches 148; Conservative 82; Mismatches 233; Indels 196; Gaps 28;

Qy	1	MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQA	STTDDDDLXLE	60
		:     :	:	
Dd	1	MNKCYALVWNVSQGCVNVVSEGSRRRGKPAGAKAAIASVLALLGATALAPA	-----YAL	54
		:     :	:	
Qy	61	PVQRTAVVLFSFRSDKEGTGEKVEDTSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE	120	
		-     -	-     -	
Dd	55	PSGGTVV-----GGSGANGEIHLSSGNLSLVNCKVKDK	85	
		- - - - -	- - - - -	



Best Local Similarity 20.9%; Pred. No. 0.0018;  
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps 30;

QY	1	MNKIYRIIWN	SALNAWVAV	SELTRNH-----TKRASATVATA--VLATLLEATVQAST	51		
Db	1	MNKAYSIIW	SHSRQAWIV	ASELARGHGFVLAKNTLLVLAVVSTIGNAFVAVNISGTVSSGG	60		
QY	52	TDDDDL	LYLEPVQRT	FAVVLFSRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDN	111		
Db	61	TVSSG-----	ETQIVYS-----	GRGNSNATVNSGGTQIVNNGGKTTATTVNSSGSQN	107		
QY	112	L-----	-----	KIKONTNENTNASSFTYSLK-----	132		
Db	108	VGTSGATIST	IVNSGGIQRV	SSGGVASATNLSSGAQNI-YNLGHASNTVIFSGGNQTIFS	166		
QY	133	---	KDLTDLTSV	GTEKLSFSA NSKNVITSDTKGLNEFAKKTAE TNGD TT VHLN-----	182		
Db	167	GGITDSTNI	SSGGQQRV	SSGGVASNTTINS-----SGAQNILSEEGAISTHSSGGNQYI	221		
QY	183	GIGSTLTDT	LLNTGATNT	VNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF	242		
Db	222	SAGANATET	IVNSGGQQRV	NSG-----AVATGTVLSGG--TQNVSSGSAISTSVY	270		
QY	243	VRTYD	TVFEFLSAD	TKTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTCCKDKGENDSS	302		
Db	271	NSGVQTV-	FAGATVTD	TTVN--SGGNQNISSGGIVSETTVNVSGTQNIYSG---GSALSA	324		
QY	303	TDKGEGLV	TAKEVIDA	VNKAGWRMKT TTANG-----QTQADKFETVTSGTNVTFASG--	355		
Db	325	NIKGSQI-	-----	VNSEGTAINTLVSDGGYQHIRNGGIIASGTIVNQSGYVNISSGGY	375		
QY	356	-----	KGTTATVSK	DDQGNITVMYD---VNVGD-ALNVNQLQNSGWNL-----DSK	397		
Db	376	AESTIINS	GGTLRLVLS	DGYARGTILNNSGRENVSGGVSYNAMINTGGNQYIYSDGEATA	435		
QY	398	AVAGSSG--	KVISGNVSP	SKGKMDETVNINAGN---NIEITRNGKNI-----DIA	442		
Db	436	AIVNTSGF	ORINSGGT	APVQNSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRCIWSNFL	495		
QY	443	TSMT	PQFSSVSL	GAGADAPTL	SVDDGALN-----VG	474	
Db	496	TAVWSM	FPGTASGA	-----NVNLSGR	LNAFAGNVVGTILNQEGRQYVYSGATATSTVG	548	
QY	475	SKDANKP	VRITNVAP	GVKEGDVTNVAQLKGV	QAQNLNNHIDNV	DGNARA-----GIAQAIA	529
Db	549	NNEGREYV	---	LSGGITDGT	VLNSGGLQAVSSG-----GKASATVINEGGAQFVY	595	
QY	530	TAGLVQAY	LPKSMMAI	GGGTYRGEAGYAIGYSSISDGGN	569		
Db	596	DGGQV----	TGTNIK--	NGGTIRVDSGASALNIALSSGGN	629		

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:53 ; Search time 19.11 Seconds  
(without alignments)  
1203.528 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWN\$ALNAWAVS.....TASGNSRGHFGASASVGQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	244	8.1	1039	1 AG43_ECOLI	P39180 escherichia
2	224	7.4	2249	1 OMPA_RICRI	P15921 rickettsia
3	219	7.3	1286	1 AIDA_ECOLI	Q03155 escherichia
4	216.5	7.2	1325	1 YDEK_ECOLI	P32051 escherichia
5	204.5	6.8	1577	1 HLYA_PROMI	P16466 proteus mir
6	203	6.7	1608	1 HLYA_SERMA	P15320 serratia ma
7	198	6.6	2003	1 YDBA_ECOLI	P33666 escherichia
8	195	6.5	1654	1 OMPB_RICRI	Q53047 r outer mem
9	195	6.5	1953	1 BIGA_SALTY	P25927 salmonella
10	194.5	6.4	933	1 SLAP_CAMFE	P35827 campylobact
11	193	6.4	2021	1 OMPA_RICCN	Q52657 rickettsia
12	192.5	6.4	1645	1 OMPB_RICTY	P96989 r outer mem
13	192.5	6.4	1655	1 OMPB_RICCN	Q9kka3 r outer mem
14	190	6.3	2334	1 WAPA_BACSU	Q07833 bacillus su
15	187	6.2	1569	1 YPJA_ECOLI	P52143 escherichia
16	180.5	6.0	918	1 YMJB_CAEEL	P34487 caenorhabdi
17	176	5.8	1228	1 SLAP_BACST	P35825 bacillus st
18	173	5.7	1300	1 120K_RICRI	P14914 rickettsia
19	172.5	5.7	1567	1 ICEN_XANCT	P18127 xanthomonas
20	172.5	5.7	3591	1 FHAB_BORPE	P12255 bordetella
21	171.5	5.7	1861	1 APU_THETU	P38536 t amylopull
22	170.5	5.6	917	1 HXA3_HAEIN	P45355 haemophilus
23	170.5	5.6	1656	1 OMPB_RICJA	O06653 r outer mem
24	169	5.6	1770	1 PMPC_CHLTR	O84419 chlamydia t
25	167	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
26	165.5	5.5	1036	1 HP12_DEIRA	P13126 deinococcus
27	165	5.5	642	1 FLID_CAMJE	Q9phw6 campylobact
28	165	5.5	928	1 HXA2_HAEIN	P45354 haemophilus
29	165	5.5	928	1 PM10_CHLPN	Q9rb65 chlamydia p
30	165	5.5	1007	1 Y741_CHLMU	Q9pj76 chlamydia m
31	164.5	5.4	1025	1 SLAP_CAUCR	P35828 caulobacter
32	163.5	5.4	1276	1 PMP6_CHLPN	Q9z899 chlamydia p
33	162.5	5.4	1167	1 CAGA_HELPJP	Q9zlt1 helicobacte

34	161	5.3	1848	1 CBPA_CLOCL	P38058 clostridium
35	160.5	5.3	671	1 ALYS_ENTFA	P37710 enterococcu
36	160.5	5.3	1310	1 VAC3_HELPY	Q48253 helicobacte
37	160.5	5.3	2476	1 ATRX_MOUSE	Q61687 mus musculu
38	159.5	5.3	2329	1 YS89_CAEEL	Q09624 caenorhabdi
39	159	5.3	550	1 FLIC_SHIFL	Q08860 shigella fl
40	158.5	5.3	1291	1 VAC4_HELPY	Q48258 helicobacte
41	158	5.2	497	1 FLIC_ECOLI	P04949 escherichia
42	158	5.2	730	1 GLN3_YEAST	P18494 saccharomyc
43	157.5	5.2	524	1 P60_LISIV	Q01837 listeria iv
44	156.5	5.2	862	1 SLA2_BACAN	P94217 bacillus an
45	155.5	5.2	1902	1 PIP_LACLC	P16271 lactococcus

ALIGNMENTS

RESULT 1	
AG43_ECOLI	
ID AG43_ECOLI STANDARD; PRT: 1039 AA.	
AC P39180; P76360; P75614; P97241; Q46771;	
DT 01-FEB-1995 (Rel. 31, Created)	
DT 01-NOV-1997 (Rel. 35, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Antigen 43 precursor (AG43) (Pluffing protein).	
GN FLU OR B2000.	
OS Escherichia coli.	
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC Escherichia.	
OX NCBI_TaxID=562;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=K12 / MG1655;	
RX MEDLINE=97426617; PubMed=9278503;	
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,	
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	
RA Mau B., Shao Y.;	
RT "The complete genome sequence of Escherichia coli K-12.";	
RL Science 277:1453-1474(1997).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=K12;	
RX MEDLINE=97251358; PubMed=9097040;	
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,	
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,	
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,	
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,	
RA Sivasubdaram S., Tagami H., Takeda J., Takemoto K., Wada C.,	
RA Yamamoto Y., Horiuchi T.;	
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome	
RT corresponding to the 40.1-50.0 min region on the linkage map.";	
RL DNA Res. 3:379-392(1996).	
RN [3]	
RP SEQUENCE FROM N.A.	
RC STRAIN=ML 308-225;	
RA Henderson I.R., Owen P.;	
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.	
RN [4]	
RP PRELIMINARY SEQUENCE OF 53-78.	
RC STRAIN=ML 308-225;	
RX MEDLINE=89291704; PubMed=2661530;	
RA Caffrey P., Owen P.;	
RT "Purification and N-terminal sequence of the alpha subunit of antigen	
RT 43, a unique protein complex associated with the outer membrane of	
RT Escherichia coli.";	
RL J. Bacteriol. 171:3634-3640(1989).	
RN [5]	
RP SEQUENCE OF 53-63.	
RC STRAIN=K12 / EMG2;	
RX MEDLINE=9743975; PubMed=9298646;	
RA Link A.J., Robison K., Church G.M.;	
RT "Comparing the predicted and observed properties of proteins encoded	



```
CC EMBL; M31227; AAA26380.1; -
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
FT SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 7.4%; Score 224; DB 1; Length 2249;
Best Local Similarity 24.2%; Pred. No. 0.001;
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

QY 13 LNAWAVSELTRN--HTKRASATVATAVLATLLFATVQASTDDDDL-----YLEPVQRT 65
DB 640 LNLGALSQVTDIGNTNSLATISVGAGTATLGGAVIKATTKITNAVS AVKFTNPVVVT 699

QY 66 AVVLSFRSDKEG---TGEKEVTEDSNWGVYFDKKGVLT-----AGTITLKAGDNLKIKON 117
DB 700 GAIDSTGNANGIVFTGNSIVTGDIG-----NTNALATVNVGAGTATL---GGAVIKAT 751

QY 118 TNENTNASSFTYSLKKDLTSLVSGTEKLSFSANSKNVNITSDTKGLNFAKKTAEANGDT 177
DB 752 TTKLTNAASVL-----TLTNANAVLTGAIDNTTGGDNVGV-----LNLGALSQVTDG- 799

QY 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNV---TDDEKKRAASVKDVLNAGWNKGVKPGT 234
DB 800 -----IGNTNSLATISVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAVDNT 853

QY 235 TASDNVDVFRTYDTVEFLSADPKTTTVNVVESKDKNGKRTEVKIGAKT-----SVIKEKDGK 289
DB 854 TGGDNVGVNLNGALSQVTDIGNT-----NSLAT-ISVGAGTATLGGAVIKATTTK 904

QY 290 L-----VTGKDKGENDSSTDKEGL 309
DB 905 LTNAASVLTLTNANAVLTGAIDNTTGGDNVGVNLNGALSQVTDG-DIGNTNSLATISVGA 963

QY 310 VTA-----KEVIDAVNKAGWRMKTTTANGQTQGADKFFETVTSCTNVTFASSGKGTATV 362
DB 964 GTATLGGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGI-VTFTGNSTVVTGNV 1022

QY 363 SKDDQGNITVMYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNSVSPSKGMDETV 422
DB 1023 -----GNTNALATVNVGAGL--LQVGGVVKANTINLTDNASAVTFTNPVVVTGAIDNTG 1075

QY 423 NINAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGAG-----ADAPTLSDVDEG 469
DB 1076 NANNGIVFTGNSVTGNVGN-----TNALATVNVGAGLLQVGGVVKANTINLTDNA 1128

QY 470 ALNVGSKDANKPVRITNVAPGVKEGDVTNVQAQLKGVAQNLNHIDNVGNARA----GIA 525
DB 1129 S-----AVFTFN--PVVVTGAIDNTG-----NANGLIVFTGNSTVTGDIGNT 1169

QY 526 QAIAT-----AGL-VQAYLPKSKMMA-----ICGGTYRGEAGYAIGY--- 561
DB 1170 NALATVNVGAGITLQA---GGSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYYFK 1220
```

```
QY 562 SSISDGGNWIILK-----GTASGNSRGH---FGASASVG 591
DB 1221 GAANGNNAILNVNTKLLTASHLTIGTVAEINIGAGNLTFTIDASVG 1266

RESULT 3
AIDA_ECOLI
ID AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC Q03155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aida-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid pIB6.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65022; CAA46156.1; -.
DR PIR; S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP ? 1286
FT SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 7.3%; Score 219; DB 1; Length 1286;
Best Local Similarity 20.9%; Pred. No. 0.001;
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps 30;

QY 1 MNKIYRIIWSALNAWAVAVSELTRNH-----TKRASATVATA--VLATLLFATVQAST 51
DB 1 MNKAYSIWHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFVAVNISGTVSSGG 60

QY 52 TDDDDLLLEPVQRTAVVLSFRSDKEGTEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDN 111
DB 61 TVSSG-----ETQIVYS-----GRGNSNATVNSGGTQIVNNGKTTATTVNSSGSQN 107

QY 112 L-----KIKONTNENTNASSFTYSLK----- 132
DB 108 VGTSGATISTIVNSGGIORVSSGGVASATNLSSGAQNI-YNLGHASNTVIFSGNQTIIFS 166

QY 133 ---KDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAEANGDTTVHLN----- 182
DB 167 GGITDSTNISSSGGQQRVSSGGVASNTTINS-----SGAQNILSEGAISTHISGGNQYI 221

QY 183 GIGSTLTDTLLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 242
DB 183 GIGSTLTDTLLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 242
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Db 222 SAGANATETIVNSGGFQRVNSG-----AVATGTVLSGG--TQNVSSGGSAISTSVY 270  
QY 243 VRTYDTVEFLSADTKTTTVNVESKDNKRGKRTVEKIGAKTSVKEKDKGLVTGDKGENDSS 302  
Db 271 NSGVQTV-FAGATVTDTTVN--SGGNQNISSGGIVSETTVNVSGTQNIYSG----GSALSA 324  
QY 303 TDKGEGLVTAKEVIDAVNKAGWRMKTITANG-----QTQADKFETVTSNTVTFASG-- 355  
Db 325 NIKGSOI-----VNSEGTAINTLVSDGGYQHIRNGGFIASGTIVNQSGVNISSGGY 375  
QY 356 -----KGTATVSKDDQGNITVMYD-----VNVGD-ALNVNQLQNSGWNL-----DSK 397  
Db 376 AESTIINSGGTLRLVSLDGYARGTILNNSGRENVSNGGVSYNAMINTGGNQVIYSDGEATA 435  
QY 398 AVAGSSG--KVISGNVSPSKGMDTETVNIAGN---NIETRNKGNI-----DIA 442  
Db 436 AIVNTSGFORINSGGTAPVQNSVVTVTVSSAAKPFDAEYVSGGKQTVVLWRGIWYSNFL 495  
QY 443 TSMTPOFSSVSLGAGADAPTLSDVDEGALN-----VG 474  
Db 496 TAVWSMFPCTASGA-----NVNLSGRLNFAFAGNVVGTILNQEGRQYVYSGATATSTVG 548  
QY 475 SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHIDNVDSGNARA-----GIAQAI 529  
Db 549 NNEGREYV----LSGGITDGTVLNSGGIQAQVSSG-----GKASATVINEGGAQPVY 595  
QY 530 TAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDSGN 569  
Db 596 DGGQV----TGTVNIK--NGGTIRVDSGASALNIALSSGNN 629  
  
RESULT 4  
YDEK\_ECOLI  
ID YDEK\_ECOLI STANDARD; PRT; 1325 AA.  
AC P32051; P76140; P77168;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical lipoprotein ydek precursor (ORF7).  
GN YDEK OR ORF7 OR B1510.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 595-1325 FROM N.A.  
RX MEDLINE=94100243; PubMed=8274505;  
RA Cartwright P.J., Timms M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;  
RT "An Escherichia coli gene showing a potential ancestral relationship  
to the genes for the mitochondrial import site proteins ISP42 and

RT MOM38.";  
RL Biochim. Biophys. Acta 1153:345-347(1993).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
CC (Potential).  
CC -!- SIMILARITY: TO E.COLI YP4L.  
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
CC ISP42 AND MOM38.  
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
CC FRAMESHIFT IN POSITION 653.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AE000248; AAC74583.1;  
DR EMBL; D90793; BAA15190.1; ALT\_INIT.  
DR EMBL; D90794; BAA15197.1; ALT\_INIT.  
DR EMBL; X73295; CAA51730.1; ALT\_FRAME.  
DR PIR; S34315; S34315.  
DR EcoGene; EG11780; ydek.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
KW Complete proteome.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
FT CONFLICT 884 884 N -> K (IN REF. 3).  
FT CONFLICT 1317 1317 M -> S (IN REF. 3).  
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;  
  
Query Match 7.2%; Score 216.5; DB 1; Length 1325;  
Best Local Similarity 23.1%; Pred. No. 0.0014;  
Matches 150; Conservative 75; Mismatches 260; Indels 165; Gaps 28;  
  
QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATAVLAATLLEATVQAATTTDDDLYLE 60  
Db 1 MNRIYRVINWCTLQVFQACSELTRRAGKTSTVNLKSSGLTTKESRL----- 47  
QY 61 PVORTAVLSFRSDKEGTGEKEVTEDS---NWGVYFDK--KGVLTAGTITLKAGDNLKI 114  
Db 48 ----TLGVLLALSGSASGASLEVDNDQITNIDTVAYDAYLVGWYGTGVNLNLAGNASL 103  
QY 115 KONTNENTNASSFTYSLKKDLTDLTSV--GPEKLSFSANSNK-VNI-TSDTKGLNFAKK- 169  
Db 104 -----TTITTSVIGANEDSEGTNVVLGGTWRLYDSGNARPLNVGQSGTGTNLNIKQK 156  
QY 170 -----TAETNGDTTVHLNGIGSTLTDLTLLNTGA---TTNVTNDNVTDDEKKRAAS 216  
Db 157 HVDGGYLRGSSSTGGVGTNVEGEDSVLTTELFEIGSYGTGSLNIT-----DKGYVTSS 210  
QY 217 VKDVLNAGWNKGVKPGTTASDNVDVFTVDTVEFLSADTKTTTVNVES-----KDNGK 270  
Db 211 IVAIL-----GYQAGSNGQ-----VVVEKGGEWLKKNDS 240  
QY 271 RTEVKIGAKTSVIKEKDKGLVTGKDKGENSDSDTKGEGLVTAKEVIDAVNKAGWRMKT 330  
Db 241 SIEFQIG-----NQGTGEATIREG-GLVTAENTIIGGNATG----IGT 278  
QY 331 ANGQTGQADKFETVTSNTVTFASGKGTATVSKDQGNITVMYDVNVGDALN--VNQLQ 388  
Db 279 LNVQ--DQDSVITVRLYNGYFGNG---TVNISNGLINNKKEYSLVGVQDGSFGVNVVD 333  
QY 389 NSGNWL-----DSKAVAGSSGKVISGNVSPSKGKMDTETVNIAGN---- 428  
Db 334 KGHWNFLGTGEAFRIYIGDAGDGLNVSSEKGVDSIITAG---MKET---GTGNITVK 387  
QY 429 --NTEITRNKGNIATIATSMTPQFSSVSLGAGADAPTLSDVDEGALNV-----GSKDANKP 481



Db 388 DKNSVITNLGTYDGHGEMNISNOGLVVSSGSSLYGETGVGNVSITTTGGMWEVNKN 447

QY 482 VRITNAPGVKEGDVTNVAQLKGAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLP-- 539

Db 448 VYTTIGVAGVGNLNIISDGG--KFVSNITFLGDKASGIGTGLNLMDATSSFDTVGINVGNF 505

QY 540 GKSMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIGKGTASGNSR 581

Db 506 GSGIVNVSGATLNTSTGYGFIGGNASGKIVNISTDSLWNLK-TSSINAQ 554

RESULT 5

HLYA\_PROMI

ID HLYA\_PROMI STANDARD; PRT; 1577 AA.

AC P16466;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hemolysin precursor.

GN HPMA.

OS Proteus mirabilis.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Proteus.

OX NCBI\_TaxID=584;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.

RC STRAIN=ISOLATE 477-12;

RX MEDLINE=90170827; PubMed=2407716;

RA Uphoff T.S., Welch R.A.;

RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpma and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shla and shlb).";

RL J. Bacteriol. 172:1206-1216(1990).

CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.

CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.

CC -!- SUBCELLULAR LOCATION: Outer membrane.

CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.

CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).

CC -----

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CC -----

DR EMBL; M30186; AAA25657.1; --.

DR PIR; A35140; A35140.

KW Hemolysis; Toxin; Outer membrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 1577 HEMOLYSIN.

SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.8%; Score 204.5; DB 1; Length 1577;

Best Local Similarity 22.6%; Pred. No. 0.0066;

Matches 149; Conservative 76; Mismatches 257; Indels 177; Gaps 30;

QY 22 LTRNHTKRASATVATAVIALTLFATVQASTDDDDLYLEPVQRTAVVLSFRSDKEGTGEK 81

Db 317 LTKTELKGNIT-----LVASSNQIKASDLMGDDITLQGADLTI-----DGKQLQOK 364

QY 82 EVTEDSNW-----GVYFDKKG---VLTAGTITL-----KAGDNLKI 114

Db 365 ETDIDNRWFYSWKYDVTKEKEIQIGSQIDAKNNATLTATKGDVTLDAKINAGNNLAI 424

QY 115 -----KQNTNENTNASSFTYSLKK-----DLTDLT----- 139

Db 425 NANKDIHINGLVEKESRSENGKNRHTSRLESWSNSHQETLTKASELTAGKDLGLDAQ 484

QY 140 -SVGTEKLSFSAANSKNVNITSDTKGLNEFAKKAETNGDITVHLN-----GIGSTLTDLL 193

Db 485 GSITAQGAKLHANENVLVNAKDNINLVQK----TNDKKTVDNHYVMGGGIGGQGNKNN 540

QY 194 NTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGK-----VKPGTTASDNVDFVRYDT 248

Db 541 NQQQVSHAT--QLTADGQLLLAADNNVNVITGSQVKGNGQAFVK--TTQGDVVIDNALSET 596

QY 249 VEFLSAD-----TKTTTVNVESKDNKRTVEKIGAKTSVIKEKD----GKLVYTGKDKG 297

Db 597 ISKIDERTGTFAPNITKSSHKNETNKQTSCTGSELISDAQLTVVSGNDVNVIGSLIKSADKL 656

QY 298 ENDSSTD---KGEGLVT-----AKEVIDAVNKAGWRMKTATTANGQTGQADK 340

Db 657 GIHSLGDINVKSAQQVTKIDDEKTSLAITGHAKEVEDKQYSAGFHITHTNKNTSTETE 716

QY 341 FETVTSGTNVTFASGKGTTATVS--KDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKA 398

Db 717 ANSTISGANVDLQANKDVTTFAGSDLKTTAGNASITGD-NVAFVSTENKKQTD--NTDTTI 773

QY 399 VAGSSGKVISGNVSPSKGKMDETVNNINAGNNEITRN-GKNIDIATSMTPQFSSVSLGAG 457

Db 774 SGGFS---YTGVDVKVGSKADFQYD-KQHTQTEVTKNRGSQTEVAGDLTITANKDLLHEG 829

QY 458 A-----DAPTLSDVDE-----GALNVG-----SKDANKPVR-----IT 485

Db 830 ASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGVNLDYSGVTKPVKKAIEDGVN 889

QY 486 NVAPGVKEGDVTNVAQLKGAQNLN--HIDNVGDNARAGI-----AQAIATA 531

Db 890 TTKPG-NNTDLTKKVTARDAIANLANLSNLETPNVGVEVGIKGGSQSQSDSQAVSTS 947

RESULT 6

HLYA\_SERMA

ID HLYA\_SERMA STANDARD; PRT; 1608 AA.

AC P15320;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hemolysin precursor.

GN SHLA.

OS Serratia marcescens.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Serratia.

OX NCBI\_TaxID=615;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.

RC STRAIN=SN8;

RX MEDLINE=88257037; PubMed=3290200;

RA Poole K., Schiebel E., Braun V.;

RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";

RT marcescens.";

RL J. Bacteriol. 170:3177-3188(1988).

CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.

CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.

CC -!- SUBCELLULAR LOCATION: Outer membrane.

CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).

CC -----

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CC -----



Db 189 IDEANN-TVALE-----GVSADGATKWQYNHNGELV-ITGDNATVNNNGKTTVDGKDSTGT 242

QY 180 HUNG-IGSTLTDTLLNT---GATTNVTNDNVNDDDEKKRAASVKDVLNAGWNIKGVPKGT 235

Db 243 EINGNNGKVIQDGLDVSGGGHIDITGDSATVD-NKGTMTVTDPESMGIQIDGDK-AIV 300

QY 236 ASDNVDFVRTVFEFLSADTKTTTVNVESKDNGK---RTEVKIGAKTSVIKEKDGL-V 291

Db 301 NNEGESTITNGTGQTINGDDATANNNGKTTVDGKDSTGT-----GNNGKVI--QDGDLDV 357

QY 292 TGKDKG---ENDSST--DKGEGLVTAKEVID-----AVNKAGWRMKTTTANGQTGQA 338

Db 358 SGGGHGIDITGDSATVDNKGTMVTDPESIGIQVDGDQAVVNEG---ESAITNGGTG-- 412

QY 339 DKFETVTSNTVFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKA 398

Db 413 ----TQINGDDAT-ANNNGKTTVDGKDSTGT-----E 439

QY 399 VAGSSGKVI-SGNVSPSKGMDETVINAGNNIEITRNGKNIDIATSMT---PQFSSVSL 454

Db 440 IAGNNGKVIQDGLDVSGG-----CHGIDITGDSATVDNKGTMVTDPE-----SI 485

QY 455 GAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNH-I 513

Db 486 GIQIDGDAIVNNEGEST-----ITNGGTG-----TQINGNDATANNNGK 525

QY 514 DNVDGNARAGIAQAIATAGLVQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI 573

Db 526 TTVDGKDSGT-TKIAGNIGIVN--LDG-SLTVTGG-----AHGVENIGDNGTVNNK 572

QY 574 GTASGNSRGHFG 585

Db 573 GDIVVSDTGSIG 584

RESULT 8

OMP\_RICRI ID OMPB\_RICRI STANDARD; PRT; 1654 AA.

AC Q53047;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein)

DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)

DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].

GN OMPB.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsieae; Rickettsia.

OX NCBI\_TaxID=783;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R;

RX MEDLINE=92167802; PubMed=1724278;

RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;

RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";

RL Mol. Microbiol. 5:2361-2370(1991).

RN [2]

RP SEQUENCE OF 279-1654 FROM N.A.

RC STRAIN=R;

RX MEDLINE=90136087; PubMed=2515418;

RA Gilmore R.D. Jr., Joste N., McDonald G.A.;

RT "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii.";

RL Mol. Microbiol. 3:1579-1586(1989).

CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

CC -----

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CC -----

DR EMBL; X16353; CAA34403.1; -.

DR InterPro; IPR003858; rOmpA\_rOmpB.

DR Pfam; PF02708; rOmpA\_rOmpB; 1.

KW Antigen; S-layer; Cell wall.

FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.

FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.

FT DOMAIN 1181 1188 POLY-THR.

SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.5%; Score 195; DB 1; Length 1654;

Best Local Similarity 21.3%; Pred. No. 0.02;

Matches 165; Conservative 93; Mismatches 273; Indels 244; Gaps 36;

QY 30 ASATVATAVLATLLFATVQ-----ASTTDDDLYLEPVQRTAVVLSFRSDKEGTGEKE 82

Db 20 STATIVASFAGSAMGAAIQQNRTTNGAATTVDGAGFDQTAAPANVGVALNA-----V 71

QY 83 VTEDSNWGVYFDK----KGVL--TAGTITLKAGDNLIKQNTNENTNASSFTYSLK--K 133

Db 72 ITANANNGINFNTPAGSFNGLLLNTANNLAVTSEDTTLGFTITNVVHNAHSFNLTLNAGK 131

QY 134 DLTLDTLSVGTEKLSFSANSNKVNI-----TSDTKGL-----NFAK 168

Db 132 TLT-ITGGQVTNAQAAATKNAQNVVQFNNGAIDNNDLKGVRIDFGAPASTLVFNLAN 190

QY 169 KTAETN---GDTTVHLNGIGSTLTD-----LLNT----- 195

Db 191 PTTQKAPLILGDNAVIANGVNGTLNVTNGFIQVNSKSFATVKAINIADGGIIFNTDANN 250

QY 196 -----GATTNVTNDNVTD-----EKKRAASVKDVLNA-GWNIKGVPKGTASDNVD 241

Db 251 ANTNLQAGGTTINFTGTDGTGRLVLLSKHAAATNFNITGSLGGLNKGVIEFNTVA---- 306

QY 242 FVRTYDTVEFLSADTKTTVN-----VESKDNGK----- 270

Db 307 -VDGQLTANAGAAANAVIGTNNAGRAAGFVVSVDNGKVATIDGQVYAKDMVIGSANATGQ 365

QY 271 ---RTEVKIGAK-TSVIKEKDKLVTKGDKGENSSTDKGEGLVTAKEVIDAV----- 319

Db 366 VNRHIVDVGADGTAFKTAASKVTITQD--SNFGNTDFG-NLAAQIKVPNAITLTGNFT 422

QY 320 -----NKAGWRMKTITANG--QTGQADKFEITVSGTNVTFASGKGT-----TATVS 363

Db 423 GDASNPGNTAG--VITFDANGTLESASADANVAVTNNITAEASGAGVVQLSGTHAAELR 480

QY 364 KDDQGNITVMYDVNVGDALN--VNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKM--- 418

Db 481 LGNAGSIFKLAD--GTVINGKVNQTALVGGALAAAGTITLDGSATITGDIGNAGGAAALQ 537

QY 419 -----DETVNINA-GNNIEITRNGKNI---DIATSMTPQFS 450

Db 538 RITLANDAKKTLTGGANIIGAGGGTIDLQANGGTIKLTSTQNNIVVDFDLAIA-TDQTG 596

QY 451 SVSLGAGADAPTLSDVDE-----GALNVGSKD---ANKPVRITNVAPGVKEGDV 496

Db 597 VVDASSLTNAQTLTINGKIGTIGANNKTLGQFNICSSKTVLSNGNVAINELVIG-NDGAV 655

QY 497 -----TNVAQLKGVAQNLNHIDNVGNARAGIAQAIATAGLVQAYLPK-----S 542

Db 656 QFAHDTYLITRRTTNAAGQCKIIFNPVVNNGTTLAAGTNLGSATNPLAEINFGSKGVNVD 715

QY 543 MMAIGGGTYRGEAGYA-----IGYSSISDGGNWIKGTASGNSRGHFGASA 588



Db 716 VLVNGEVNLT-----YATNITTTDANVGSEFVENAGGTNIIVSGTVGGQQGNKFNNTVA 766

RESULT 9

BIGA\_SALTY STANDARD; PRT; 1953 AA.

AC P25927; P25928; Q9XCQ3;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Putative surface-exposed virulence protein bigA precursor.

GN BIGA OR STM3478.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI\_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=14028;

RA Stojiljkovic I., Valentine P., Heffron F.;

RT "Salmonella typhimurium rhs homolog.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";

RT Nature 413:852-856(2001).

RL [3]

RN SEQUENCE OF 1-765 FROM N.A.

RP STRAIN=LT2;

RC MEDLINE=91100301; PubMed=1987123;

RX Wu J.Y., Siegel L.M., Kredich N.M.;

RA "High-level expression of Escherichia coli NADPH-sulfite reductase: requirement for a cloned cysG plasmid to overcome limiting shroheme cofactor.";

RT J. Bacteriol. 173:325-333(1991).

RL -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.

CC -----

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CC -----

DR EMBL; AF133696; AAD39458.1; -.

DR EMBL; AE008859; AAL22340.1; -.

DR EMBL; M64606; AAA27042.1; ALT\_FRAME.

DR EMBL; M64606; AAA27043.1; ALT\_FRAME.

DR PIR; C39200; C39200.

DR PIR; D39200; D39200.

DR StyGene; SGI0437; bigA.

KW Virulence; Repeat; Signal; Complete proteome.

FT SIGNAL 1 27

FT CHAIN 28 1953

FT PUTATIVE SURFACE-EXPOSED VIRULENCE

FT PROTEIN BIGA.

FT 15 X 11 AA TANDEM REPEATS.

FT REPEAT 101 252

FT REPEAT 101 103

FT REPEAT 104 113

FT REPEAT 114 122

FT REPEAT 123 133

FT REPEAT 134 144

FT REPEAT 145 155

FT REPEAT 156 166 7.

FT REPEAT 167 177 8.

FT REPEAT 178 188 9.

FT REPEAT 189 199 10.

FT REPEAT 200 210 11.

FT REPEAT 211 221 12.

FT REPEAT 222 232 13.

FT REPEAT 233 243 14.

FT REPEAT 244 252 15 (INCOMPLETE).

FT CONFLICT 207 207 D -> DRGDDDDVTPDD (IN REF. 1).

FT CONFLICT 514 514 A -> R (IN REF. 3).

FT CONFLICT 1698 1698 D -> N (IN REF. 1).

FT CONFLICT 1795 1798 QYLE -> ITLQ (IN REF. 1).

FT CONFLICT 1836 1837 SA -> T (IN REF. 1).

SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match 6.5%; Score 195; DB 1; Length 1953;

Best Local Similarity 21.7%; Pred. No. 0.025;

Matches 141; Conservative 81; Mismatches 232; Indels 196; Gaps 33;

QY 41 TLLFATVQASTTDDDDLLYLEPQVQRTAVVLS-FRSDKEGTGEKEVTE----- 85

Db 347 TVISGDDQAHNS-DRGMDISGQDRTGTVIISGDRVTNLTGSSVTDGATGMVISGDGTTN 405

QY 86 -----DSNWGVYFDKKGVLT-----AGTILKAGDNLKIKONTNENTNASSF 127

Db 406 TISGHSTVDNATGALISGNGTTTNFAGDIAVSGGGTAIIDGNATIK-----NTGTS-- 458

QY 128 TYSLKKDLTDLTSVGTGTEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGDITVHLNGIGST 187

Db 459 -----DISGAGSTGTVIDGNNAVRN-----NDGDMTITDGGTGGH 493

QY 188 LT-DTLL--NTGATT-----NVTNDNVTDDEKKRAASVKDVLNAG-WNIKGKPKGT 234

Db 494 ITGDNVVIDNAGSTTVSGADATALLYIEGDNAL-----VINEGNTISGGAVGT 541

QY 235 TA-SDNVDFVRTYDVEFLSADTKTTVNVESKDNKRTEVKIGAKTSVIKEKDGLVTG 293

Db 542 RIDGDDAHTTNTGD----IAVDGAGSAAVIINGDNGSLTQA-----GDLLV- 583

QY 294 KDKGENSSTDKGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVTSNTVTF- 352

Db 584 -----TDGAMGIITYGTGNEAKN-----TGNATVRDADSVGFVAVAGEKNTFK 625

QY 353 -----ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKV 406

Db 626 NKGDIDVSLNGTGALVS-GDMSQVTLGDGINV---VSVQDSEGVFSSATGVSVSGDSNAV 681

QY 407 -ISGNVSPS-----KGKMDFTVINAGNNIETRNGK-NI---DIATSMTPQPSV 452

Db 682 DITGNVNISADYGQDDLAAGAPPLTGVVVGNGNTVTLNGALNIDNDLSATGGQYLDVV 741

QY 453 SLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKVAQNLNH 512

Db 742 GLSVTGDDNDVEID--GGINI--THSEDPLDGT-----ADITGISVSGNSTVTLNH 790

QY 513 IDNVGDNARAG-----IAQAIATAGLV-----QAYLP-----GKSMMAIGGGTYR 552

Db 791 -STIDTNTVVGHHVVLARVNNGGSLILGDDSVVDVNVSYIPTGYTYTNALLMADGEGTSI 849

QY 553 GEAG-----YAI-----GYSSISDGGNWIICKGTASGNSRGHFGASASVG 591

Db 850 ENKGDITSHGVISVIRADNGSEVNSGDIIVYATSSNSEDRAITRASG 899

RESULT 10

SLAP\_CAMFE

ID SLAP\_CAMFE STANDARD; PRT; 933 AA.

AC P35827;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)











CC CC SIMILARITY).

CC CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR

CC CC (BY SIMILARITY).

CC CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-

CC CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).

CC CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

CC CC -----

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CC CC -----

DR EMBL; AE008659; AAL03623.1; -

DR EMBL; AF123721; AAF34124.1; -

DR EMBL; AF123726; AAF34129.1; -

DR EMBL; AF149110; AAD39533.1; -

DR InterPro; IPR003858; rOmpA\_rOmpB.

DR Pfam; PF02708; rOmpA\_rOmpB; 1.

KW Antigen; S-layer; Cell wall; Complete proteome.

FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.

FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.

FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).

FT CONFLICT 353 354 KD -> GH (IN REF. 3).

FT CONFLICT 776 776 F -> S (IN REF. 3).

FT CONFLICT 1159 1159 E -> D (IN REF. 3).

FT CONFLICT 1177 1177 G -> S (IN REF. 3).

FT CONFLICT 1492 1492 H -> R (IN REF. 3).

SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 6.4%; Score 192.5; DB 1; Length 1655;

Best Local Similarity 22.4%; Pred. No. 0.027;

Matches 149; Conservative 78; Mismatches 283; Indels 155; Gaps 31;

QY 10 NSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLLYLEPVQRTAVVL 69

Db 211 NGTLN-----VTNGFIKVSRSKFATVNVINIGDQGQIMFNTDADNVNTLNQANGATI 263

QY 70 SFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLK--IKQNT----- 118

Db 264 TP-NGTDGTGRL-----VLLSKNAAATDFNVGTSLGGLNKGIIEFNTVAVNGOLKA 313

QY 119 NENTNASSFTYSLKKDLTDLTSVGTEK-----LSFSANSNKV-----NITSDTKGLNF 166

Db 314 NAGANAA-----VIGTNNGAGRAAGFVVVDNGKVATIDGQVYAKDMVIQS 359

QY 167 AKKTAETNGDTHVHLNGIGSLTDLTLLNTGATNTVNDNVTDDEKKRAASVKD---VLNA 223

Db 360 ANAVGQVNFRIHVVDGTDGTTAFKTAASKVAITQNSNFGTTDFGNLAAQIIIVPNTMTLNG 419

QY 224 GWNIGKVKPGTASDNVDFVRYD--TVEFLSADTKTTTVN-----VESKDNG----- 269

Db 420 NFTGDASNPGNTAG-----VITFDANGTLASASADANVAVTNNTAIEASGAGVVQLSGT 474

QY 270 KRTEVKIGAKTSVIKEKDGKLVGKDKGENSDSDKGEGLVTAKEVIDAVNKAGWRMKT 329

Db 475 HAAELRLGNAGSVFKLADGTVINGK---VNQTALVGGALAAGTITLDG-----SA 521

QY 330 TANGQTGQA-----DKFETVT-----SCFNVTFAASKGTGTATVSKDDQ 367

Db 522 TITGDIGNAGAAALQGITLANDATKTLTLCGANIIGANGGTINFGANGGTIKLTS--TQ 579

QY 368 GNITVMYDV-----NVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKM-D 419

Db 580 NNIVVDFDLAIATDQTVGDASSLTNAQTLTINGKIGTVGANKTKLGQFNIGSSKTVLSD 639

QY 420 ETYNIN--AGNN--IEITRNGKNIDIAATSMTPQ----FSSV-----SLGAGADAPTLSV 465

Db 640 GDVAINELVINGNGAVQFAHNTYLTTRTTNAAGCGKIIFNPVVNNNTTLATGTNLGS-AT 698

QY 466 DDEGALNVGSKDANKPVRITNVAPGVKEGDVTNYAQLKGVAQNLLNNHIDNVG-NARAGI 524

Db 699 NFLAEINFGSKGAANVDTVLVNCKGVNL-YATNITTTDA---NVGSFIFNAGGTNIIVSG- 753

QY 525 AQAATATAGLVQ-----AYLPCKSMMAIGGGYRGEAGYAIGYSSISDGGNWIILKTAS 577

Db 754 -----TVGGQCGNKFKENTVALDNGTTVTKFLGNAFNGNTTIAAN-STLQIGGNYTADFVAS 807

QY 578 GNSRG 582

Db 808 ADGTG 812

RESULT 14

WAPA\_BACSU

ID WAPA\_BACSU STANDARD; PRT; 2334 AA.

AC Q07833;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Wall-associated protein precursor.

GN WAPA OR N17G.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI\_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=93302506; PubMed=8316082;

RA Foster S.J.;

RT "Molecular analysis of three major wall-associated proteins of

RT Bacillus subtilis 168: evidence for processing of the product of a

RT gene encoding a 258 kDa precursor two-domain ligand-binding

RT protein.";

RL Mol. Microbiol. 8:299-310(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168 / BGSC1A1;

RX MEDLINE=95219088; PubMed=7704263;

RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis

RT genome containing the hut and wapa loci.";

RL Microbiology 141:337-343(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=168 / BGSC1A1;

RX MEDLINE=97124196; PubMed=8969509;

RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,

RA Miwa Y., Fujita Y.;

RT "Sequencing of a 65 kb region of the Bacillus subtilis genome

RT containing the lic and cel loci, and creation of a 177 kb contig

RT covering the gnt-sacXY region.";

RL Microbiology 142:3113-3123(1996).

CC -!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,

CC MOTILITY, SECRETION OR DIFFERENTIATION.

CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED

CC INTO THE MEDIUM.

CC -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE

CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE

CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED

CC MOTIF REPEATED 31 TIMES.

CC -!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME

CC SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHS-A-D).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration





DR	EMBL; D90889; BAA16514.1; ALT_INIT.
DR	EMBL; D90890; BAA16518.1; ALT_INIT.
DR	EcoGene; EG13213; ypjA.
KW	Hypothetical protein; Outer membrane; Complete proteome.
SQ	SEQUENCE 1569 AA; 162774 MW; OD006A9A32154596 CRC64;
Query Match	
Best Local Similarity 6.2%; Score 187; DB 1; Length 1569;	
Matches 152; Conservative 87; Mismatches 262; Indels 232; Gaps 35;	
QY	41 TLLFAIVQASTTDDDDLYLEPVQRTAVVLSFRSDKEGT-----GEKEVTEDSNWGVYFD 94
Db	534 TVVAKTSAKNTTIDTGGKL-IVQKEAKTDSLRLNNGVLEVDGGGEAKHVEQQSGGALI- 591
QY	95 KKGVLTAGTI---TLKAGDNLKIKONTNENT---NASSFT----- 128
Db	592 --ASTTSGTLIEGTNSYGDIFYIRNSEAKNVVLENAGSLTVVTCRAVDTIINANGKMDV 649
QY	129 YSLKKDL-TDLTSVGTSEKLSFSANSKNVNITSDTK---GL-----NFAKKTAEFTNGDFT-- 178
Db	650 YG--KDVGTVLNSAGTQTIYASATSDKANIKGKQTVYGLATEANIESGEQIVDGGSTEK 707
QY	179 VHLNG-----IGSTLTDTLLNTG-----ATTNVTNDN 205
Db	708 THINGGTQTVQNYGKAINTDIVSGLOQIMANGTAEGSIINGGSQVVVNEGGLAENSVLNDG 767
QY	206 VTDD--EKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVTYDTVEFLSADTKTTTV-- 261
Db	768 GTLDVREKGSATGIQ-----SSOGALVATTRATRVGTGRA-DGVAFSEQGAANNILL 820
QY	262 -----NVESKDNGKRTEVKIGAKTSVJEK-----DGKL 290
Db	821 ANGGVLTVESDTSDDKTQVNMGGR-EIVKTKATATGTLTGGEQIVEGVANETTINDGGI 879
QY	291 VTGKDKGENDSSTDKGEGLVTAKE---VIDAVNKAGWRMKTTTANGQTQADKFETVTSG 347
Db	880 QTVSANGEAIKTKINEGGTLTVNDNGKATDIVQNSGAALQTSTANG-----IEISG 930
QY	348 TNV--TFASGKGTATVSKDDQGNITVWYDVNVGDAL--NVNQLQNSGWNLDKAVAGSS 403
Db	931 THQYGTFSISGNLATNMLLENGGNLLVLAGTEARDSTVKGKGAMONLG--QDSATKVNSG 988
QY	404 GKVISGNVSPSKGKMDETVINAGNNIEITRNGKNIDIATS-----MTPQ----- 448
Db	989 GQYTLGRSKDEFQALARAEDLQVAGGTAIVYAGTLADASVSGATGSLSLMTPRDNVTPVK 1048
QY	449 -----FSSVSLGAGADA--PTLSVDDEGALNVGSKD-----ANKPVRITNVAPGVK 492
Db	1049 LEGAVRITDSATLTGLNGVDFTLADLTAASRGSVWLNSNNSCAGTSNCEYRVNSLL--LN 1106
QY	493 EGDV-----TNVAQLKGVAQNLNHNHIDNVDGN 519
Db	1107 DGDVYLSAQTAAPATTNGIYNTLTITNELSGSGNFYLTHTNVAGSRGDLVVNN---NATGN 1163
QY	520 ARAGIAQAATAGLVQAYLPKGSMMMAIGGTYRGEAGYAIG-----YSSISDG 567
Db	1164 FKI----FVQDTGVSPQSDDAMTLVKTTGG----GDASFILGNTGGFVDLGTYEYVLKSDG 1215
QY	568 -GNWIIKGTASGN 579
Db	1216 NSNWNLNTNDVKPN 1228

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:18 ; Search time 55.9 Seconds  
(without alignments)  
1838.265 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 3019  
Sequence: 1 MNKIYRIIWNALSALNAWAVS.....TASGNSRGHFGASASVG YQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues 562222  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SPTREMBL\_19:\*
  - 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3019	100.0	594	2	Q93QY4	Q93qy4 neisseria m
2	2931	97.1	594	2	Q9JPI3	Q9jpi3 neisseria m
3	2927	97.0	594	2	Q9JPS2	Q9jps2 neisseria m
4	2874	95.2	594	2	Q9JPH7	Q9jph7 neisseria m
5	2863	94.8	598	2	Q9JPR9	Q9jpr9 neisseria m
6	2861	94.8	598	2	Q9JPT0	Q9jpt0 neisseria m
7	2855	94.6	598	2	Q9JPS0	Q9jps0 neisseria m
8	2852	94.5	598	2	Q93QY5	Q93qy5 neisseria m
9	2806	92.9	600	2	Q9JPS6	Q9jps6 neisseria m
10	2790	92.4	590	2	Q9JPS3	Q9jps3 neisseria m
11	2762.5	91.5	599	2	Q9JPR8	Q9jpr8 neisseria m
12	2758.5	91.4	591	2	Q9JPS7	Q9jps7 neisseria m
13	2758.5	91.4	591	16	Q9JRI8	Q9jri8 neisseria m
14	2751	91.1	592	2	Q9AQF0	Q9aqf0 neisseria m
15	2739.5	90.7	591	2	Q93QY3	Q93qy3 neisseria m
16	2736.5	90.6	599	2	Q9JPS8	Q9jps8 neisseria m

17	2718	90.0	598	2	Q9JPR7	Q9jpr7 neisseria m
18	2678	88.7	592	2	Q9JPS9	Q9jps9 neisseria m
19	2655.5	88.0	595	2	Q9JPH0	Q9jph0 neisseria m
20	2636	87.3	592	2	Q93QY2	Q93qy2 neisseria m
21	2606	86.3	600	2	Q9JPS5	Q9jps5 neisseria m
22	2533	83.9	592	16	Q9JQW4	Q9jqw4 neisseria m
23	2527.5	83.7	589	2	Q9JPI0	Q9jpi0 neisseria m
24	2516.5	83.4	589	2	Q93QY1	Q93qy1 neisseria m
25	2444.5	81.0	526	2	Q9JPS4	Q9jps4 neisseria m
26	2442.5	80.9	530	2	Q9JPS1	Q9jps1 neisseria m
27	1328.5	44.0	2353	2	P71401	P71401 haemophilus
28	1030	34.1	1098	2	Q48152	Q48152 haemophilus
29	423	14.0	1299	16	Q9F3X6	Q9f3x6 pasteurella
30	398.5	13.2	2059	16	Q9PD50	Q9pd50 xylella fas
31	384.5	12.7	1190	16	Q9PC04	Q9pc04 xylella fas
32	384.5	12.7	2712	16	Q9F3X5	Q9f3x5 pasteurella
33	375.5	12.4	1107	2	Q9F2D8	Q9fd8 salmonella
34	263	8.7	1291	16	Q92KQ7	Q92kg7 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98hj2 rhizobium l
36	244	8.1	1039	2	Q9L6T7	Q9l6t7 escherichia
37	243	8.0	2276	2	Q93TY6	Q93ty6 staphylococ
38	239	7.9	1004	16	Q9PD63	Q9pd63 xylella fas
39	236	7.8	1039	2	Q9L6T8	Q9l6t8 escherichia
40	230	7.6	1040	2	Q9AL50	Q9al50 shigella fl
41	228.5	7.6	1265	2	Q9FDA0	Q9fda0 xanthomonas
42	228.5	7.6	1557	2	Q9RNI2	Q9rni2 haemophilus
43	224.5	7.4	989	2	Q9XD84	Q9xd84 escherichia
44	223	7.4	1213	16	Q98JH8	Q98jh8 rhizobium l
45	222	7.4	1018	16	Q9HWU6	Q9hwu6 pseudomonas

ALIGNMENTS

RESULT 1

Q93QY4					
ID	Q93QY4	PRELIMINARY;	PRT;	594	AA.
AC	Q93QY4;				
DT	01-DEC-2001 (Tremblrel. 19, Created)				
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)				
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)				
DE	NHHA OUTER MEMBRANE PROTEIN.				
GN	NHHA.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=EG327;				
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;				
RT	"Identification and characterization of a gene encoding a novel outer				
RT	membrane protein of Neisseria meningitidis.";				
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF157605; AAK68866.1; ..				
SQ	SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;				

Query Match 100.0%; Score 3019; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKIYRIIWNALSALNAWAVSELTRNHTKRASATVATAVATLTLFATVQASTTDDDDLYLE	60
Db	1	MNKIYRIIWNALSALNAWAVSELTRNHTKRASATVATAVATLTLFATVQASTTDDDDLYLE	60
QY	61	PVQRTAVVLSFRSDKEGTGEKVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE	120
Db	61	PVQRTAVVLSFRSDKEGTGEKVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE	120
QY	121	NTNASSFTYSLKKDLTDLTSGVTEKLSFSANSKNVNITSDTKGLNFAKKTAEINGDTTVH	180
Db	121	NTNASSFTYSLKKDLTDLTSGVTEKLSFSANSKNVNITSDTKGLNFAKKTAEINGDTTVH	180

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QY 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
Db 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKDKKGEND 300
Db 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKDKKGEND 300
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVTSGTNVTFASGKGTTA 360
Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVTSGTNVTFASGKGTTA 360
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
QY 421 TVNINAGNNIEITRNGKNIDIAATSMPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
Db 421 TVNINAGNNIEITRNGKNIDIAATSMPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
QY 481 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNHHDNVGDNARAGIAQAIAATAGLVQAYLPG 540
Db 481 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNHHDNVGDNARAGIAQAIAATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHGFGASASVGYOW 594
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHGFGASASVGYOW 594

RESULT 2
Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR EMBL; AF226369; AAF42518.1; -.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
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Query Match 97.1%; Score 2931; DB 2; Length 594;  
Best Local Similarity 97.1%; Pred. No. 5.6e-115;  
Matches 577; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTNE 120
Db 61 PVORTAPVLSFHADSEGTGEKTEVSDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTDE 120
QY 121 NTNASSFTYSLKKDLTDLTSVTEKLSFNSANSKNVNITSDTKGLNFAKKTAEETNGDTTVH 180
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Db 121 NTNASSFTYSLKKDLTDLTSVTEKLSFGANGKKVNITSDTKGLNFAKETAGTNGDTTVH 180
QY 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
Db 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKDKKGEND 300
Db 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKDKKGEND 300
QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVTSGTNVTFASGKGTTA 360
Db 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVTSGTNVTFASGKGTTA 360
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
Db 361 TVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
QY 421 TVNINAGNNIEITRNGKNIDIAATSMPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
Db 421 TVNINAGNNIEITRNGKNIDIAATSMPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
QY 481 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNHHDNVGDNARAGIAQAIAATAGLVQAYLPG 540
Db 481 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNHHDNVGDNARAGIAQAIAATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHGFGASASVGYOW 594
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHGFGASASVGYOW 594

RESULT 3
Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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Query Match 97.0%; Score 2927; DB 2; Length 594;  
Best Local Similarity 97.0%; Pred. No. 8.2e-115;  
Matches 576; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
Db 1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTNE 120
Db 61 PVORTAPVLSFHADSEGTGEKTEVSDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTDE 120
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RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H15;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226381; AAF42530.1; -.
DR EMBL; AF157607; AAK68868.1; -.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B88A63CB CRC64;

Query Match          94.6%; Score 2855; DB 2; Length 598;
Best Local Similarity 94.6%; Pred. No. 8.2e-112;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
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Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60

QY 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTNE 120
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Db 61 PVQRTAVVLSFRSDKEGTGEKTEVDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120

QY 121 NTNA-----SSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEINGD 176
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Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSEFGANGKNVNTSDTKGLNFAKETAGTNGD 180

QY 177 TTVHLNGIGSTLTDLLNTGATTNVNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTGA 236
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Db 181 PTVHLNGIGSTLTDLLNTGATTNVNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTGA 240

QY 237 SDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTGDK 296
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Db 241 SDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTGKGK 300

QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGK 356
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Db 301 DENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGN 360

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 420

QY 417 KMDETVINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
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Db 421 KMDETVINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDVNDGNARAGIAQAIATAGLVQA 536
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Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDVNDGNARAGIAQAIATAGLAQA 540

QY 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVGYQW 594
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Db 541 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGHFGASASVGYQW 598

RESULT 8
Q93QY5 ID Q93QY5 PRELIMINARY; PRT; 598 AA.
AC Q93QY5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=B210;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157603; AAK68864.1; -.
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match          94.5%; Score 2852; DB 2; Length 598;
Best Local Similarity 94.6%; Pred. No. 1.1e-111;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
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Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60

QY 61 PVORTAVVLSFRSDKEGTGEKTEVDSNWGVYFDKKGVLTAAGTITLKAGDNLKIKONTNE 120
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Db 61 PVORTAVVLSFRSDKEGTGEKTEVDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120

QY 121 NTNA-----SSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEINGD 176
   |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSEFGANGKNVNTSDTKGLNFAKETAGTNGD 180

QY 177 TTVHLNGIGSTLTDLLNTGATTNVNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTGA 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 PTVHLNGIGSTLTDLLNTGATTNVNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTGA 240

QY 237 SDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTGDK 296
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 SDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKRTVEVKIGAKTSVIKEKDGLVTGKGK 300

QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGK 356
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Db 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGN 360

QY 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
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Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG 420

QY 417 KMDETVINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
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Db 421 KMDETVINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

QY 477 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDVNDGNARAGIAQAIATAGLVQA 536
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Db 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDVNDGNARAGIAQAIATAGLAQA 540

QY 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVGYQW 594
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGHFGTSASVGYQW 598

RESULT 9
Q9JPS6 ID Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
```



RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226371; AAF42520.1. --  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match	92.9%;	Score 2806;	DB 2;	Length 600;
Best Local Similarity	92.7%;	pred. NO. 9.1e-110;		
Matches 557;	Conservative 14;	Mismatches 22;	Indels 8;	Gaps 2;

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RESULT 10  
Q9JPS3  
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.

GN	GN592.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487;
RN	[1]

RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match	92.4%;	Score 2790;	DB 2;	Length 590;
Best Local Similarity	93.5%;	Pred. No. 4.1e-109;		
Matches 557; Conservative	12;	Mismatches 19;	Indels	

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RESULT 11  
Q9JPR8

ID	Q9JPR8	PRELIMINARY;	PRT;	599 AA.
AC	Q9JPR8;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation)			
DE	OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE GNA992 OR NHHA.			
GN	GNA992 OR NHHA.			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; beta subdivision;			



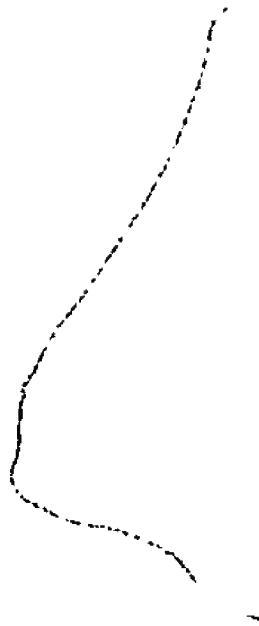




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QY	236	ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGKD	295
Db	235	ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGKTSVIKEKDGLVTGKD	294
QY	296	KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNVTFASG	355
Db	295	KGENSSTDGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNVTFASG	354
QY	356	KGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	415
Db	355	KGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK	414
QY	416	GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS	475
Db	415	GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALNVGS	473
QY	476	KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHNHIDNVVDGNARAGIAQAIAATAGLVQ	535
Db	474	KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHNRIDNVVDGNARAGIAQAIAATAGLVQ	533
QY	536	AYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	594
Db	534	AYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	592
RESULT 15			
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ID	Q93QY3	PRELIMINARY;	PRT; 591 AA.
AC	Q93QY3;		
DT	01-DEC-2001 (TReMBLrel. 19, Created)		
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)		
DE	NHHA OUTER MEMBRANE PROTEIN.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EG329;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis.";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF157606; AAK68867.1; -.		
SQ	SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;		
Query Match 90.7%; Score 2739.5; DB 2; Length 591;			
Best Local Similarity 91.8%; Pred. No. 5.3e-107;			
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;			
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QY	58	YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ	116
Db	61	YLDPVLRVAVLIVNSDKEGTGEKEVEENS DWAYVFNEKGVLTAREITLKAGDNLKIKQ	120
QY	117	NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAETNGD	176
Db	121	-----NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGD	174
QY	177	TTVHLNGIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIIKGVKPGTTA	236
Db	175	TTVHLNGIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIIKGVKPGTTA	234
QY	237	SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGLVTGKD	296

Db	235	SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVIKEKDGLVTGKDK	294
QY	297	GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNVTFASGK	356
Db	295	GENSSTDGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNVTFASGK	354
QY	357	GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG	416
Db	355	GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKG	414
QY	417	KMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK	476
Db	415	KMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALNVGSK	473
QY	477	DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHNHIDNVVDGNARAGIAQAIAATAGLVQA	536
Db	474	KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNHNRIDNVVDGNARAGIAQAIAATAGLVQA	533
QY	537	YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	594
Db	534	YLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	591

Search completed: September 5, 2002, 10:30:29  
Job time: 431 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:24:43 ; Search time 58.77 Seconds  
(without alignments)  
1122.645 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 15  
Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	594	100.0	594	20	AAU23740
2	594	100.0	594	21	AAU57044
3	594	100.0	594	22	AAU06174
4	161	27.1	407	22	AAU06184
5	161	27.1	433	22	AAU06185
6	161	27.1	502	22	AAU06186
7	161	27.1	512	22	AAU06182
8	161	27.1	591	20	AAU27202
9	161	27.1	591	20	AAU23741
10	161	27.1	591	20	AAU23746
11	161	27.1	591	21	AAU57045
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					BASB029 amino acid
					N. meningitidis EG
					N. meningitidis PM
					N. meningitidis PM
					N. meningitidis PM
					N. meningitidis PM
					Amino acid sequenc
					A surface protein
					BASB029 amino acid

12	161	27.1	591	22	AAU06171	N. meningitidis PM
13	161	27.1	591	22	AAU06175	N. meningitidis EG
14	161	27.1	592	20	AAU23737	A surface protein
15	138	23.2	513	22	AAU06183	N. meningitidis H4
16	138	23.2	589	20	AAU23745	A surface protein
17	138	23.2	589	22	AAU06173	N. meningitidis P2
18	138	23.2	592	20	AAU23744	A surface protein
19	138	23.2	592	22	AAU06172	N. meningitidis H4
20	138	23.2	598	20	AAU23738	A surface protein
21	138	23.2	598	20	AAU23742	A surface protein
22	138	23.2	598	22	AAU06177	N. meningitidis H1
23	138	23.2	598	22	AAU06178	N. meningitidis B2
24	127	21.4	592	20	AAU27203	Amino acid sequenc
25	127	21.4	592	22	AAU06180	N. meningitidis Z2
26	98	16.5	245	20	AAU27201	Amino acid sequenc
27	94	15.8	599	20	AAU23743	A surface protein
28	94	15.8	599	22	AAU06176	N. meningitidis H3
29	93	15.7	594	20	AAU23739	A surface protein
30	93	15.7	594	22	AAU06179	N. meningitidis B2
31	82	13.8	116	21	AAU37832	Neisserial conserv
32	72	12.1	72	21	AAU37830	Neisserial conserv
33	59	9.9	604	22	AAU06181	N. meningitidis su
34	43	7.2	53	21	AAU37828	Neisserial conserv
35	32	5.4	56	21	AAU37827	Neisserial conserv
36	23	3.9	1098	17	AAU99392	Haemophilus adhesi
37	22	3.7	2353	17	AAU99393	Haemophilus adhesi
38	22	3.7	2411	21	AAU23860	Haemophilus influe
39	20	3.4	20	21	AAU37831	Neisserial conserv
40	19	3.2	19	21	AAU51546	Yada homologous pe
41	19	3.2	19	21	AAU51547	Yada homologous pe
42	18	3.0	1004	21	AAU23857	Haemophilus influe
43	17	2.9	17	21	AAU37818	Neisserial conserv
44	17	2.9	1094	21	AAU23858	Haemophilus influe
45	16	2.7	16	21	AAU37819	Neisserial conserv
46	16	2.7	16	21	AAU37829	Neisserial conserv
47	15	2.5	15	21	AAU37822	Neisserial conserv
48	15	2.5	15	21	AAU37825	Neisserial conserv
49	15	2.5	23	21	AAU37824	Neisserial conserv

ALIGNMENTS

RESULT 1

AAU23740

ID AAY23740 standard; Protein; 594 AA.

XX

AC AAY23740;

XX

DT 08-SEP-1999 (first entry)

XX

DE A surface protein of Neisseria meningitidis.

XX

KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

XX

OS Neisseria meningitidis.

XX

PN WO9931132-A1.

XX

PD 24-JUN-1999.

XX

PF 14-DEC-1998; 98WO-AU01031.

XX

PR 12-DEC-1997; 97GB-0026398.

XX

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU ) UNIV QUEENSLAND.

XX

PI Jennings MP, Moxon ER, Peak IRA;

XX

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

XX	Neisseria meningitidis surface proteins useful for treating N. meningitidis infections	
PT	Claim 1; Page 100-101; 132pp; English.	
XX	The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.	
XX	Sequence 594 AA;	
SQ		
Query Match 100.0%; Score 594; DB 20; Length 594;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60	
Db	1 mnkiyriiwnsalnawavseltrnhtkrasatvataviatlffatvgastddddlyle 60	
QY	61 PVQRTAVVLSFRSDKEGTGEKTEVDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120	
Db	61 pvqrtavvlsfrsdkegtgektevdsnwgyvfdkkgvltagtitlkagdnlkikqntne 120	
QY	121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFNSANSKNVNITSDPKGLNFAKKTAEETNGDTTVH 180	
Db	121 ntnassfty slkkdltdltsvgteklsfsansknvnitsdtkglnfakktaeetngdttvh 180	
QY	181 LNGIGSTLTDTLLNTGATNTVNDVTDEKKRAASVKDVLNAGWNKGVKPGTASDNV 240	
Db	181 lngigstltdtllntgattvndvndtdekkraasvkdvlmagwnikgvpkpgttasdnv 240	
QY	241 DFVRTYDTVEFLSADTKTTTVNVESKDKGRKTEVKIGAKTSVIKEKDGKLVTKDKGEND 300	
Db	241 dfvrttydtveflsadtktttvnveskdngkrtevkigaktvikekdgklvtgdkgend 300	
QY	301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFEVTSCTNVTFAFGKGTGA 360	
Db	301 sstdkgeglvtakevidavnkagwrmtttangqtgqadkfevtsgtnvtfasgkgtta 360	
QY	361 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGKMD 420	
Db	361 tvskddqgnitvm ydvnvgd alnvnqlqns gwnldskavagssgkvisgnvsp skgkmd 420	
QY	421 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480	
Db	421 tvninagnieitrngknidiat smtpqfssvslgagadap tlvdd egalnv gskdank 480	
QY	481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNNHIDNVGNARAGIAQAIAATAGLVQAYLPG 540	
Db	481 pvr itnv apgvkegdvtnvaqlkgvaqnl nhdnvdgnarag iaqaiataglvqaylpg 540	
QY	541 KSMAIAGGTYRGEAGYALGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594	
Db	541 ksmaia ggtyrgeag yaigyssisd ggnwi kgtas gnsrghfgas asvgyqw 594	
RESULT	2	
AA57044		
XX	AA57044 standard; Protein; 594 AA.	
AC	AA57044;	
XX		
DT	21-FEB-2000 (first entry)	
XX		
DE	BASB029 amino acid sequence from N. meningitidis strain ATCC13090.	

XX	BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.	
KW	Neisseria meningitidis.	
XX		
OS		
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 104 /note= "Encoded by AATC"	
XX		
PN	WO9958683-A2.	
XX		
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999; 99WO-EP03255.	
XX		
PR	13-MAY-1998; 98GB-0010276.	
XX		
PA	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.	
XX	Ruelle J;	
PI		
XX	WPI; 2000-053103/04.	
DR	N-PSDB; AAZ39864.	
XX		
PT	New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal	
XX	Claim 4; Fig 2; 74pp; English.	
XX	This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-239865) and polypeptide sequences (AA57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.	
XX	Sequence 594 AA;	
SQ		

Query Match 100.0%; Score 594; DB 21; Length 594;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60	
Db	1 mnkiyriiwnsalnawavseltrnhtkrasatvataviatlffatvgastddddlyle 60	
QY	61 PVQRTAVVLSFRSDKEGTGEKTEVDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120	
Db	61 pvqrtavvlsfrsdkegtgektevdsnwgyvfdkkgvltagtitlkagdnlkikqntne 120	
QY	121 NTNASSFTYSLKKDLTDLTSVGTSEKLSFNSANSKNVNITSDPKGLNFAKKTAEETNGDTTVH 180	
Db	121 ntnassfty slkkdltdltsvgteklsfsansknvnitsdtkglnfakktaeetngdttvh 180	
QY	181 LNGIGSTLTDTLLNTGATNTVNDVTDEKKRAASVKDVLNAGWNKGVKPGTASDNV 240	
Db	181 lngigstltdtllntgattvndvndtdekkraasvkdvlmagwnikgvpkpgttasdnv 240	



Db 481 pvrlnvapgkdvtnvaqlkgvaqnlhndvgnaraglaqaiataglvqaylpq 540

QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
|||||

Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594  
|||||

RESULT 4

AAU06184

ID AAU06184 standard; Protein; 407 AA.

XX

AC AAU06184;

XX

DT 24-OCT-2001 (first entry)

XX

DE N. meningitidis PMC21 Nhha deletion mutant #2.

XX

KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;

KW mutant; mutein.

XX

OS Neisseria meningitidis strain PMC21.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1..51

FT /label= Signal\_peptide

FT Protein 52..407

FT /label= Mature\_Nhha\_deletion\_mutant\_#2

FT /note= "Predicted mature protein, specifically

FT claimed in claim 12"

XX

PN WO200155182-A1.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-AU000069.

XX

PR 25-JAN-2000; 2000US-0177917.

XX

PA (UYQU ) UNIV QUEENSLAND.

XX

PI Peak IRA, Jennings MP;

XX

DR WPI; 2001-488774/53.

DR N-PSDB; AAS09174.

XX

XX New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 12; Fig 7; 9lpp; English.

XX

CC The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence represents N. meningitidis strain PMC21 surface

CC antigen Nhha deletion mutant #2.

XX

SQ Sequence 407 AA;

Query Match 27.1%; Score 161; DB 22; Length 407;

Best Local Similarity 100.0%; Pred. NO. 1.1e-149;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTttTANGQTQADKFETVTSgTNVTFASGKGTTATYSKD 365

Db 120 geglvtakevidavnkagwrmttttangqtgqadkfetvtsgtnvtfasgkgtatvskd 179  
|||||

QY 366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVTISGNVSPSKGMDETVNIN 425  
|||||

Db 180 dqgnitvmynvgdalnvnqlqnswnldskavagssgkvsgnvnpsksgkmdetvnn 239  
|||||

QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466  
|||||

Db 240 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 280  
|||||

RESULT 5

AAU06185

ID AAU06185 standard; Protein; 433 AA.

XX

AC AAU06185;

XX

DT 24-OCT-2001 (first entry)

XX

DE N. meningitidis PMC21 Nhha deletion mutant #3.

XX

KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;

KW mutant; mutein.

XX

OS Neisseria meningitidis strain PMC21.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1..51

FT /label= Signal\_peptide

FT Protein 52..433

FT /label= Mature\_Nhha\_deletion\_mutant\_#3

FT /note= "Predicted mature protein, specifically

FT claimed in claim 12"

XX

PN WO200155182-A1.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-AU000069.

XX

PR 25-JAN-2000; 2000US-0177917.

XX

PA (UYQU ) UNIV QUEENSLAND.

XX

PI Peak IRA, Jennings MP;

XX

DR WPI; 2001-488774/53.

DR N-PSDB; AAS09175.

XX

XX New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 12; Fig 8; 9lpp; English.

XX

CC The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence represents N. meningitidis strain PMC21 surface

CC antigen Nhha deletion mutant #3.

XX

SQ Sequence 433 AA;



```
Query Match      27.1%; Score 161; DB 22; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTATVSKD 365
    |||||
Db 146 geglvtakevidavnkagwrmktttangtggadkfetvtsgtntvfaskgttatvskd 205
    |||||

QY 366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425
    |||||
Db 206 dqgnitvmydvnvgdalnvqnqlnsgwnldskavagssgkvisgnvpskkgmdetvnin 265
    |||||

QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
    |||||
Db 266 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 306
    |||||

RESULT 6
AAU06186
ID AAU06186 standard; Protein; 502 AA.
XX
AC AAU06186;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #4.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..49
FT /label= Signal_peptide
FT Protein 50..502
FT /label= Mature_Nhha_deletion_mutant_#4
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09176.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 12; Fig 9; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
```

```
CC antigen Nhha deletion mutant #4.
XX
SQ Sequence 502 AA;

Query Match      27.1%; Score 161; DB 22; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.3e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTATVSKD 365
    |||||
Db 215 geglvtakevidavnkagwrmktttangtggadkfetvtsgtntvfaskgttatvskd 274
    |||||

QY 366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425
    |||||
Db 275 dqgnitvmydvnvgdalnvqnqlnsgwnldskavagssgkvisgnvpskkgmdetvnin 334
    |||||

QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
    |||||
Db 335 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 375
    |||||

RESULT 7
AAU06182
ID AAU06182 standard; Protein; 512 AA.
XX
AC AAU06182;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #1.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..512
FT /label= Mature_Nhha_deletion_mutant_#1
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09172.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 12; Fig 5; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
```

CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen NhhA deletion mutant #1.  
XX

SQ Sequence 512 AA;  
  
Query Match 27.1%; Score 161; DB 22; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.3e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKFFETVTSGTNVTFASGKGTTATVSKD 365  
Db 225 geglvtakevidavnkagwrmttttangtgqadkfetvtsgtntvfaskggtatvskd 284  
  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
Db 285 dqgnitvmydvnvgdalnvnglqnswnldskavagssgkvvisgnvpskkgmdetvnin 344  
  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
Db 345 agnieitrngknidiatsmtpqfssvslgagadaptilsvd 385

RESULT 8  
AAAY27202  
ID AAY27202 standard; Protein; 591 AA.  
XX  
AC AAY27202;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9936544-A2.  
XX  
PD 22-JUL-1999.  
XX  
PF 14-JAN-1999; 99WO-IB00103.  
XX  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX  
PA (CHIR-) CHIRON SPA.  
XX

PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
XX  
DR WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX

CC The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisserial  
CC bacteria, especially Neisseria meningitidis.  
XX

SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKFFETVTSGTNVTFASGKGTTATVSKD 365  
Db 304 geglvtakevidavnkagwrmttttangtgqadkfetvtsgtntvfaskggtatvskd 363  
  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
Db 364 dqgnitvmydvnvgdalnvnglqnswnldskavagssgkvvisgnvpskkgmdetvnin 423  
  
QY 426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
Db 424 agnieitrngknidiatsmtpqfssvslgagadaptilsvd 464

RESULT 9  
AAAY23741  
ID AAY23741 standard; Protein; 591 AA.  
XX  
AC AAY23741;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85793.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 104-106; 132pp; English.  
XX

CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX

SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 21; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTATVSKD 365  
|||||

Db 304 geglvtakevidavnkagwrmttttangqtgqadkfetvtsgtntvfaskgttatvskd 363  
|||||

QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425  
|||||

Db 364 dqgnitvmydvnvgdalnvnglqnsqwnldskavagsgkvisgnvpskqkmdetvnn 423  
|||||

QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466  
|||||

Db 424 agnnieitrngknidiatsmtppqfssvslgagadaptlsvd 464  
|||||

RESULT 12

AAU06171

ID AAU06171 standard; Protein; 591 AA.

XX AAU06171;

DT 24-OCT-2001 (first entry)

XX N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

OS Neisseria meningitidis strain PMC21.

XX Key Location/Qualifiers

FT Peptide 1..51

FT /label= Signal\_peptide

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..108

FT /label= V1

FT /note= "Variable region 1"

FT Protein 52..591

FT /label= Mature\_Nhha

FT /note= "Predicted mature protein, specifically

FT Region 109..120

FT /label= C2

FT /note= "Conserved region 2"

FT Region 121..124

FT /label= V2

FT /note= "Variable region 2"

FT Region 125..188

FT /label= C3

FT /note= "Conserved region 3"

FT Region 189..210

FT /label= V3

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FT /label= C4

FT /note= "Conserved region 4"

FT Region 230..236

FT /label= V4

FT /note= "Variable region 4"

FT Region 237..591

FT /label= C5

FT /note= "Conserved region 5"

XX WO200155182-A1.  
PN  
XX  
PD  
XX  
PF 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU000069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09161.  
XX

PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX

PS Claim 9; Fig 1; 9lpp; English.

XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX

SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 22; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 364 dqgnitvmydvnvgdalnvnglqnsqwnldskavagsgkvisgnvpskqkmdetvnn 423  
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QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466  
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Db 424 agnnieitrngknidiatsmtppqfssvslgagadaptlsvd 464  
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RESULT 13

AAU06175

ID AAU06175 standard; Protein; 591 AA.

XX AAU06175;

AC AAU06175;

XX 24-OCT-2001 (first entry)

XX N. meningitidis EG329 surface antigen Nhha polypeptide sequence.

DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain EG329.

OS Neisseria meningitidis strain EG329.

XX Key Location/Qualifiers

FT Region 1..50





Thu Sep 5 14:35:47 2002

Db 425 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 465  
RESULT 15  
AAU06183  
ID AAU06183 standard; Protein; 513 AA.  
XX  
AC AAU06183; ~  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis H41 Nhha deletion mutant.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.  
XX  
OS Neisseria meningitidis strain H41.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= signal\_peptide  
FT 52..513  
FT Protein /label= Mature\_Nhha\_deletion\_mutant  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"  
XX  
WO200155182-A1.  
PN  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
WPI; 2001-488774/53.  
DR N-PSDB; AAS09173.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 6; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain H41 surface  
XX antigen Nhha deletion mutant.  
SQ Sequence 513 AA;

Search completed: September 5, 2002, 10:31:59  
Job time: 436 sec

Query Match 23.2%; Score 138; DB 22; Length 513;  
Best Local Similarity 100.0%; Pred. No. 5.9e-127;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 434 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:28:13 ; Search time 25.6 Seconds  
(without alignments)  
566.750 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALSALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 15

Total number of hits satisfying chosen parameters: 41

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
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5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	594	100.0	594	4	US-09-377-155-9	Sequence 9, Appli
2	594	100.0	594	4	US-09-669-974-9	Sequence 9, Appli
3	161	27.1	591	4	US-09-377-155-11	Sequence 11, Appl
4	161	27.1	591	4	US-09-377-155-21	Sequence 21, Appl
5	161	27.1	591	4	US-09-669-974-11	Sequence 11, Appl
6	161	27.1	591	4	US-09-669-974-21	Sequence 21, Appl
7	161	27.1	592	4	US-09-377-155-2	Sequence 2, Appli
8	161	27.1	592	4	US-09-669-974-2	Sequence 2, Appli
9	138	23.2	589	4	US-09-377-155-19	Sequence 19, Appl
10	138	23.2	589	4	US-09-669-974-19	Sequence 19, Appl
11	138	23.2	592	4	US-09-377-155-17	Sequence 17, Appl
12	138	23.2	592	4	US-09-669-974-17	Sequence 17, Appl
13	138	23.2	598	4	US-09-377-155-5	Sequence 5, Appli
14	138	23.2	598	4	US-09-377-155-13	Sequence 13, Appl
15	138	23.2	598	4	US-09-669-974-5	Sequence 5, Appli
16	138	23.2	598	4	US-09-669-974-13	Sequence 13, Appl
17	94	15.8	599	4	US-09-377-155-15	Sequence 15, Appl
18	94	15.8	599	4	US-09-669-974-15	Sequence 15, Appl
19	93	15.7	594	4	US-09-377-155-7	Sequence 7, Appli
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21	23	3.9	658	1	US-08-409-995-5	Sequence 5, Appli
22	23	3.9	658	3	US-08-685-467-5	Sequence 5, Appli
23	23	3.9	658	4	US-08-913-942-5	Sequence 5, Appli
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29	23	3.9	1098	4	US-09-268-347-44	Sequence 44, Appl
30	22	3.7	1912	1	US-08-409-995-4	Sequence 4, Appli
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32	22	3.7	2353	4	US-09-377-155-33	Sequence 33, Appl
33	22	3.7	2353	4	US-08-913-942-4	Sequence 4, Appli
34	22	3.7	2353	4	US-09-669-974-33	Sequence 33, Appl
35	22	3.7	2354	4	US-09-268-347-47	Sequence 47, Appl
36	22	3.7	2411	4	US-09-268-347-36	Sequence 36, Appl
37	20	3.4	607	1	US-08-409-995-6	Sequence 6, Appli
38	20	3.4	607	3	US-08-685-467-6	Sequence 6, Appli
39	20	3.4	607	4	US-08-913-942-6	Sequence 6, Appli
40	18	3.0	1004	4	US-09-268-347-30	Sequence 30, Appl
41	17	2.9	1094	4	US-09-268-347-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 594

RESULT 2  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 100.0%; Score 594; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVATAVLATL L LFATVQASTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGV L TAGTITLKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGV L TAGTITLKAGDNLKIKQNTNE 120  
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Db 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSA NSKNVNITSDTKGLNFAKKTAE TNGDTTVH 180  
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Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTS GNTVTFASGKGTTA 360  
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QY 481 PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNNHIDNV DGNARAGIAQAIATAGLVQAYLPG 540  
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RESULT 3  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 27.1%; Score 161; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTS GNTVTFASGKGTTATVSKD 365  
Db 304 GEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTS GNTVTFASGKGTTATVSKD 363  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMD ETVNIN 425  
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QY 426 AGNNIEITRNGKNIDIIATSMTPQFSSVSLGAGADAPTL SV D 466  
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RESULT 4  
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; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 27.1%; Score 161; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
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Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 5
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 27.1%; Score 161; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 363
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QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
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Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 6
US-09-669-974-21
; Sequence 21, Application US/09669974

; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 27.1%; Score 161; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 365
|
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 363
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
|
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466
|
Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464

RESULT 7
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 27.1%; Score 161; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 365
|
Db 305 GEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 364

[illegible][illegible]

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RESULT      8
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

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Query Match 27.1%; Score 161; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 306 GEGLVTAKEVIDAVNKAGWRMKT<sup>T</sup>TANGQTGQADKPE<sup>T</sup>VTS<sup>G</sup>TNTVFASGKGTTATVSKD 365  
|||||  
|||||  
**Dd** 305 GEGLVTAKEVIDAVNKAGWRMKT<sup>T</sup>TANGQTGQADKPE<sup>T</sup>VTS<sup>G</sup>TNTVFASGKGTTATVSKD 364  
|||||  
|||||

[illegible]

Qy	426	AGNNIEITRGNKNDIATSMTPQFSSVSLGAGADAP	466
D6	425	AGNNIEITRGNKNDIATSMTPQFSSVSLGAGADAP	465

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RESULT          9
US-09-377-155-19
; Sequence 19, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19

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; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-19

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Query Match 23.2%; Score 138; DB 4; Length 589;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	374	YDVNVGDALNVNQ	LQNSGWNLD	SKAVAGSSGKVI	SGNVSPP	SKGKMDETV	NINAGNNIEIT	4333
D <sub>b</sub>	369	YDVNVGDALNVNQ	LQNSGWNLD	SKAVAGSSGKVI	SGNVSPP	SKGKMDETV	NINAGNNIEIT	4288
QY	434	RNGKNIDIATSM	TPOFSSVSLGAGADAPT	LSVDDEGALNVGSKDANKPVRITNVAPGVKE	4933			
D <sub>b</sub>	429	RNGKNIDIATSM	TPOFSSVSLGAGADAPT	LSVDDEGALNVGSKDANKPVRITNVAPGVKE	4888			
QY	494	GDVTNVAQLKGVAQN	LNN 511					
D <sub>b</sub>	489	GDVTNVAOLKGVAQN	LNN 506					

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RESULT 10
US-09-669-974-19
; Sequence 19, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: prt
; ORGANISM: Neisseria meningitidis
US-09-669-974-19

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Query Match      23.2%; Score 138; DB 4; Length 589;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	374	YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVIISGNVSPSKGKMDETVNIAGNNIET	433
Db	369	YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVIISGNVSPSKGKMDETVNIAGNNIET	428
Qy	434	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE	493
Db	429	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE	488
Qy	494	GDVTNVAQLKGVAQNINN	511
Db	489	GDVTNVAQLKGVAQNINN	506

RESULT 11  
US-09-377-155-17  
; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Ansell



; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

Query Match 23.2%; Score 138; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
Db 372 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431

QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 493
Db 432 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 491

QY 494 GDVTNVAQLKGVAQNLLN 511
Db 492 GDVTNVAQLKGVAQNLLN 509

RESULT 12
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match 23.2%; Score 138; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
Db 372 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431

QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 493
Db 432 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 491

Db 432 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 491

QY 494 GDVTNVAQLKGVAQNLLN 511
Db 492 GDVTNVAQLKGVAQNLLN 509

RESULT 13
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 23.2%; Score 138; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
Db 378 YDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 437

QY 434 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 493
Db 438 RGNKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTITNVAPGVKE 497

QY 494 GDVTNVAQLKGVAQNLLN 511
Db 498 GDVTNVAQLKGVAQNLLN 515

RESULT 14
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

	Query Match	23.2%;	Score 138;	DB 4;	Length 598;
	Best Local Similarity	100.0%;	Pred. No. 2e-122;		
	Matches 138;	Conservative	0;	Mismatches	0;
				Indels	Gaps
QY	374	YDVNVGDALNVNLQNSGWNLD	SKAVAGSSGK	VISGNVSPSKGKMD	ETVNIINAGNNIEIT 433
Db	378	YDVNVGDALNVNLQNSGWNLD	SKAVAGSSGK	VISGNVSPSKGKMD	ETVNIINAGNNIEIT 437
QY	434	RNGKNIDIA	TSMTPQFSSVSLGAGADAPT	LSVDD	EGALNVGSKDANKPVRITNVAPGVKE 493
Db	438	RNGKNIDIA	TSMTPQFSSVSLGAGADAPT	LSVDD	EGALNVGSKDANKPVRITNVAPGVKE 497
QY	494	GDVTNVAQLKGV	QAQLNN	511	
Db	498	GDVTNVAQLKGV	QAQLNN	515	

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RESULT 15
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

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	Query Match	23.2%;	Score 138;	DB 4;	Length 598;
	Best Local Similarity	100.0%;	Pred. No. 2e-122;		
	Matches 138;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	374	YDYNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIEIT	433		
Db	378	YDYNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIEIT	437		
QY	434	RNGKNIDIIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE	493		
Db	438	RNGKNIDIIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE	497		
QY	494	GDVTNVAQLKGVAQNINN 511			
Db	498	GDVTNVAQLKGVAQNINN 515			

Search completed: September 5, 2002, 10:32:32  
Job time: 259 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:29:43 ; Search time 33.86 Seconds  
(without alignments)  
1685.678 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWN\$ALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 15

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	161	27.1	591	2 G81133	adhesin NMB0992 [i
2	127	21.4	592	2 A81888	probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: G81133  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755  
A;Accession: G81133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-591 <TET>  
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0992

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 8.7e-156;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFFETVTSCTNVTTFASGKGTTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFFETVTSCTNVTTFASGKGTTATVSKD 363  
|||||  
  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423  
|||||  
  
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTL\$VD 466  
|||||  
Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTL\$VD 464  
|||||

RESULT 2  
A81888

probable surface fibril protein NMAL200 [imported] - Neisseria meningitidis (strain 2  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C;Accession: A81888  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A;Reference number: A81775; MUID:20222556  
A;Accession: A81888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-592 <PAR>  
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMAL200

Query Match 21.4%; Score 127; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 5e-121;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFFETVTSCTNVTTFASGKGTTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFFETVTSCTNVTTFASGKGTTATVSKD 363  
|||||  
  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423  
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QY 426 AGNNIEI 432  
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Db 424 AGNNIEI 430

Search completed: September 5, 2002, 10:33:11  
Job time: 208 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:32:38 ; Search time 19.19 Seconds  
(without alignments)  
1198.510 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: September 5, 2002, 10:39:36  
Job time: 418 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:32:03 ; Search time 55.9 Seconds  
(without alignments)  
1838.265 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHFCASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 15

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

- Database : SPTREMBL\_19:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match %		Length	DB	ID	Description
1	594	100.0		594	2	Q93QY4	Q93qy4 neisseria m
2	221	37.2		594	2	Q9JPI3	Q9jpi3 neisseria m
3	221	37.2		594	2	Q9JPS2	Q9jps2 neisseria m
4	221	37.2		595	2	Q9JPH0	Q9jph0 neisseria m
5	162	27.3		592	2	Q9JPS9	Q9jps9 neisseria m
6	162	27.3		598	2	Q9JPR7	Q9jpr7 neisseria m
7	162	27.3		599	2	Q9JPS8	Q9jps8 neisseria m
8	161	27.1		591	2	Q9JPS7	Q9jps7 neisseria m
9	161	27.1		591	2	Q93QY3	Q93qy3 neisseria m
10	161	27.1		591	16	Q9JRI8	Q9jri8 neisseria m
11	161	27.1		592	2	Q9AQF0	Q9aqf0 neisseria m
12	138	23.2		589	2	Q9JPI0	Q9jpi0 neisseria m
13	138	23.2		589	2	Q93QY1	Q93qy1 neisseria m
14	138	23.2		590	2	Q9JPS3	Q9jps3 neisseria m
15	138	23.2		592	2	Q93QY2	Q93qy2 neisseria m
16	138	23.2		598	2	Q9JPT0	Q9jpt0 neisseria m

17	138	23.2	598	2	Q9JPS0	Q9jps0 neisseria m				
18	138	23.2	598	2	Q93QY5	Q93qy5 neisseria m				
19	138	23.2	600	2	Q9JPS5	Q9jps5 neisseria m				
20	127	21.4	592	16	Q9JQW4	Q9jqw4 neisseria m				
21	94	15.8	599	2	Q9JPR8	Q9jpr8 neisseria m				
22	93	15.7	526	2	Q9JPS4	Q9jps4 neisseria m				
23	93	15.7	530	2	Q9JPS1	Q9jps1 neisseria m				
24	93	15.7	594	2	Q9JPH7	Q9jph7 neisseria m				
25	93	15.7	598	2	Q9JPR9	Q9jpr9 neisseria m				
26	93	15.7	600	2	Q9JPS6	Q9jps6 neisseria m				
27	23	3.9	1098	2	Q48152	Q48152 haemophilus				
28	22	3.7	2353	2	P71401	P71401 haemophilus				

ALIGNMENTS

RESULT 1

Q93QY4

ID Q93QY4 PRELIMINARY; PRT; 594 AA.

AC Q93QY4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE NHHA OUTER MEMBRANE PROTEIN.

GN NHHA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EG327;

RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF157605; AAK68866.1; -.

SQ SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;

Query Match 100.0%; Score 594; DB 2; Length 594;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60

Db 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60

QY 61 PVQRTAVVLSFRSDKGEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120

Db 61 PVQRTAVVLSFRSDKGEKTEVEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120

QY 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAETNGDTTVH 180

Db 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAETNGDTTVH 180

QY 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240

Db 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240

QY 241 DFVRTYDTVEFLSADTKTTTVNVEESKDKNGKRTVEKIGAKTSVIKEKDGLVTGDKDKGEND 300

Db 241 DFVRTYDTVEFLSADTKTTTVNVEESKDKNGKRTVEKIGAKTSVIKEKDGLVTGDKDKGEND 300

QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSGTNVTFASGKGTTA 360

Db 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSGTNVTFASGKGTTA 360

QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420

Db 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMD 420

QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480

Db	421	TVNINAGNNIETRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK	480
Qy	481	PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPG	540
Db	481	PVRITNVAPGVKEGDTVNTVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPG	540
Qy	541	KSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
Db	541	KSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
RESULT	2		
Q9JPI3			
ID	Q9JPI3	PRELIMINARY;	PRT; 594 AA.
AC	Q9JPI3;		
DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NG3/88, AND BZ232;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226376; AAF42525.1; -.		
DR	EMBL; AF226369; AAF42518.1; -.		
SQ	SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;		
Query Match	37.2%;	Score 221;	DB 2; Length 594;
Best Local Similarity	100.0%;	Pred. No. 4e-204;	
Matches	221;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	374	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT	433
Db	374	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT	433
Qy	434	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE	493
Db	434	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE	493
Qy	494	GDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRG	553
Db	494	GDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRG	553
Qy	554	EAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
Db	554	EAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
RESULT	3		
Q9JPS2			
ID	Q9JPS2	PRELIMINARY;	PRT; 594 AA.
AC	Q9JPS2;		
DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		

OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NGE31;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226379; AAF42528.1; -.		
SQ	SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;		
Query Match	37.2%;	Score 221;	DB 2; Length 594;
Best Local Similarity	100.0%;	Pred. No. 4e-204;	
Matches	221;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	374	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT	433
Db	374	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT	433
Qy	434	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE	493
Db	434	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE	493
Qy	494	GDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRG	553
Db	494	GDVTNVAQLKGVAQNLNHIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRG	553
Qy	554	EAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
Db	554	EAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	594
RESULT	4		
Q9JPH0			
ID	Q9JPH0	PRELIMINARY;	PRT; 595 AA.
AC	Q9JPH0;		
DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=528, AND 1000;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226360; AAF42509.1; -.		
DR	EMBL; AF226356; AAF42505.1; -.		
SQ	SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;		



Query Match		37.2%;	Score 221;	DB 2;	Length 595;
Best Local Similarity		100.0%;	Pred. No. 4e-204;		
Matches 221;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	374	YDVNVGDALNVNQLNSGWNLD	SKAVAGSSGKVISGNVSPSKGKMD	ETVNVINAGNNIEIT	433
Db	375	YDVNVGDALNVNQLNSGWNLD	SKAVAGSSGKVISGNVSPSKGKMD	ETVNVINAGNNIEIT	434
QY	434	RNGKNIDIATSMTPQFSSVSLGAGAD	APTLSDVDD	EGALNVGSKDANKPVRIT	NAVPGVKE 493
Db	435	RNGKNIDIATSMTPQFSSVSLGAGAD	APTLSDVDD	EGALNVGSKDANKPVRIT	NAVPGVKE 494
QY	494	GDVTNVAQLKGVAQNLNH	IDNVGNARAGIAQA	IATAGLVQAYLPGKSMMA	IGGGTYRG 553
Db	495	GDVTNVAQLKGVAQNLNH	IDNVGNARAGIAQA	IATAGLVQAYLPGKSMMA	IGGGTYRG 554
QY	554	EAGYAIGYSSISDGGNWI	IKGTASGNSRGHFGASASV	GYQW 594	
Db	555	EAGYAIGYSSISDGGNWI	IKGTASGNSRGHFGASASV	GYQW 595	
RESULT 5					
Q9JPS9					
ID	Q9JPS9	PRELIMINARY;		PRT;	592 AA.
AC	Q9JPS9;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=860800;				
RC	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;				
RT	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
DR	EMBL; AF226361; AAF42510.1; -.				
SQ	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;				
Query Match		27.3%;	Score 162;	DB 2;	Length 592;
Best Local Similarity		100.0%;	Pred. No. 3e-147;		
Matches 162;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	306	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGOTGQADKFETV	TSGTNVTFASGKGTTATVSKD	365
Db	304	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGOTGQADKFETV	TSGTNVTFASGKGTTATVSKD	363
QY	366	DQGNITVMYDVNVGDALNV	NQLNSGWNLD	SKAVAGSSGKVISGNVSPSKG	KMDETVNNIN 425
Db	364	DQGNITVMYDVNVGDALNV	NQLNSGWNLD	SKAVAGSSGKVISGNVSPSKG	KMDETVNNIN 423
QY	426	AGNNIEITRNGKNIDIAT	SMTPQFSSVSLGAGAD	APTLSDVDD 467	
Db	424	AGNNIEITRNGKNIDIAT	SMTPQFSSVSLGAGAD	APTLSDVDD 465	
RESULT 6					
Q9JPR7					
ID	Q9JPR7	PRELIMINARY;		PRT;	598 AA.
AC	Q9JPR7;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				

Query Match		27.3%;	Score 162;	DB 2;	Length 598;
Best Local Similarity		100.0%;	Pred. No. 3e-147;		
Matches 162;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	306	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGOTGQADKFETV	TSGTNVTFASGKGTTATVSKD	365
Db	310	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGOTGQADKFETV	TSGTNVTFASGKGTTATVSKD	369
QY	366	DQGNITVMYDVNVGDALNV	NQLNSGWNLD	SKAVAGSSGKVISGNVSPSKG	KMDETVNNIN 425
Db	370	DQGNITVMYDVNVGDALNV	NQLNSGWNLD	SKAVAGSSGKVISGNVSPSKG	KMDETVNNIN 429
QY	426	AGNNIEITRNGKNIDIAT	SMTPQFSSVSLGAGAD	APTLSDVDD 467	
Db	430	AGNNIEITRNGKNIDIAT	SMTPQFSSVSLGAGAD	APTLSDVDD 471	
RESULT 7					
Q9JPS8					
ID	Q9JPS8	PRELIMINARY;		PRT;	599 AA.
AC	Q9JPS8;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A22;				
RC	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;				
RT	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
DR	EMBL; AF226364; AAF42513.1; -.				
SQ	SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;				
Query Match		27.3%;	Score 162;	DB 2;	Length 599;



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[3]
RN  SEQUENCE FROM N.A.
RP  SPECIES=N.meningitidis; STRAIN=PMC21;
RA  Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT  "Identification and characterization of a gene encoding a novel outer
RT  membrane protein of Neisseria meningitidis.";
RL  Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF226375; AAF42524.1; -.
DR  EMBL; AE002450; AAF41395.1; -.
DR  EMBL; AF226367; AAF42516.1; -.
DR  EMBL; AF226370; AAF42519.1; -.
DR  EMBL; AF226374; AAF42523.1; -.
DR  EMBL; AF157611; AAK68872.1; -.
DR  TIGR; NMB0992; -.
KW  Complete proteome.
SQ  SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match      27.1%; Score 161; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  306 GEGLVTAKEVIDAVNKAGWRMKT TT TANGQTQADKFETVTS GNTVTFASGKGTATVSKD 365
Db  |||||||
QY  304 GEGLVTAKEVIDAVNKAGWRMKT TT TANGQTQADKFETVTS GNTVTFASGKGTATVSKD 363
Db  |||||||

QY  366 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 425
Db  |||||||
QY  364 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 423
Db  |||||||

QY  426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVD 466
Db  |||||||
QY  424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVD 464
Db  |||||||

RESULT 11
Q9AQF0 ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match      27.1%; Score 161; DB 2; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  306 GEGLVTAKEVIDAVNKAGWRMKT TT TANGQTQADKFETVTS GNTVTFASGKGTATVSKD 365
Db  |||||||
QY  305 GEGLVTAKEVIDAVNKAGWRMKT TT TANGQTQADKFETVTS GNTVTFASGKGTATVSKD 364
Db  |||||||

QY  366 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 425
Db  |||||||
QY  365 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 424
Db  |||||||

QY  426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVD 466
Db  |||||||
QY  425 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVD 465
Db  |||||||
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RESULT 12
Q9JPIO ID Q9JPIO PRELIMINARY; PRT; 589 AA.
AC Q9JPIO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP165, 90/18311, AND 93/4286;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226384; AAF42533.1; -.
DR EMBL; AF226362; AAF42511.1; -.
DR EMBL; AF226363; AAF42512.1; -.
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match      23.2%; Score 138; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  374 YDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNINAGNNIEIT 433
Db  |||||||
QY  369 YDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNINAGNNIEIT 428
Db  |||||||

QY  434 RNGKNIDIATSMTPQFSSVSLGAGADAP TLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
Db  |||||||
QY  429 RNGKNIDIATSMTPQFSSVSLGAGADAP TLSVDDEGALNVGSKDANKPVRITNVAPGVKE 488
Db  |||||||

QY  494 GDVTNVAQLKGVAQNLNN 511
Db  |||||||
QY  489 GDVTNVAQLKGVAQNLNN 506
Db  |||||||

RESULT 13
Q93QY1 ID Q93QY1 PRELIMINARY; PRT; 589 AA.
AC Q93QY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P20;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157610; AAK68871.1; -.
SQ SEQUENCE 589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;
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Query Match 23.2%; Score 138; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433  
|||||  
Db 369 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 428  
|||||

QY 434 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 429 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 488  
|||||

QY 494 GDVTNVAQLKGVAQNLLN 511  
|||||  
Db 489 GDVTNVAQLKGVAQNLLN 506  
|||||

RESULT 14

Q9JPS3 PRELIMINARY; PRT; 590 AA.

AC Q9JPS3;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Conanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226378; AAF42527.1; -. 8AA476AC300D80C8 CRC64;  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 590;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433  
|||||  
Db 370 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 429  
|||||

QY 434 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 430 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 489  
|||||

QY 494 GDVTNVAQLKGVAQNLLN 511  
|||||  
Db 490 GDVTNVAQLKGVAQNLLN 507  
|||||

RESULT 15

Q93QY2 PRELIMINARY; PRT; 592 AA.

AC Q93QY2;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.

GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H41;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157609; AAK68870.1; -. F9403A0B4A18EEA7 CRC64;  
SQ SEQUENCE 592 AA; 61869 MW; F9403A0B4A18EEA7 CRC64;

Query Match 23.2%; Score 138; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 4e-124;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433  
|||||  
Db 372 YDVNVGDALNVNQLQNSGWNLDISKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431  
|||||

QY 434 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493  
|||||  
Db 432 RNgKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 491  
|||||

QY 494 GDVTNVAQLKGVAQNLLN 511  
|||||  
Db 492 GDVTNVAQLKGVAQNLLN 509  
|||||

Search completed: September 5, 2002, 10:39:11  
Job time: 428 sec





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:31:59 ; Search time 58.77 Seconds  
(without alignments)  
1116.975 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASVGVQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 15

Total number of hits satisfying chosen parameters: 48

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

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	2:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*		
	3:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*		
	4:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*		
	5:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*		
	6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*		
	7:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*		
	8:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*		
	9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*		
	10:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*		
	11:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*		
	12:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*		
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	14:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*		
	15:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*		
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	19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*		
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	21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*		
	22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	20	AA1980
2	573	97.0	591	20	AA1981
3	573	97.0	591	22	AAU06171
4	525	88.8	591	20	AA1982
5	525	88.8	591	22	AAU06175
6	458	77.5	512	22	AAU06182
7	432	73.1	592	20	AA1983
8	381	64.5	433	22	AAU06185
9	367	62.1	591	21	AA1984
10	355	60.1	407	22	AAU06184
11	355	60.1	502	22	AAU06186

12	175	29.6	245	20	AA1980	Amino acid sequenc
13	161	27.2	594	20	AA1981	A surface protein
14	161	27.2	594	21	AA1982	BASB029 amino acid
15	161	27.2	594	22	AAU06174	N. meningitidis EG
16	137	23.2	592	20	AA1983	Amino acid sequenc
17	137	23.2	592	22	AAU06180	N. meningitidis 22
18	117	19.8	594	20	AA1984	A surface protein
19	117	19.8	594	22	AAU06179	N. meningitidis B2
20	117	19.8	598	20	AA1985	A surface protein
21	117	19.8	598	22	AAU06177	N. meningitidis H1
22	116	19.6	116	21	AA1986	Neisserial conserv
23	116	19.6	599	20	AA1987	A surface protein
24	116	19.6	599	22	AAU06176	N. meningitidis H3
25	103	17.4	513	22	AAU06183	N. meningitidis H4
26	103	17.4	592	20	AA1988	A surface protein
27	103	17.4	592	22	AAU06172	N. meningitidis H4
28	93	15.7	589	20	AA1989	A surface protein
29	93	15.7	589	22	AAU06173	N. meningitidis P2
30	93	15.7	598	20	AA1990	A surface protein
31	93	15.7	598	22	AAU06178	N. meningitidis B2
32	72	12.2	72	21	AA1991	Neisserial conserv
33	59	10.0	604	22	AAU06181	N. meningitidis su
34	56	9.5	56	21	AA1992	Neisserial conserv
35	53	9.0	53	21	AA1993	Neisserial conserv
36	23	3.9	23	21	AA1994	Neisserial conserv
37	20	3.4	20	21	AA1995	Neisserial conserv
38	19	3.2	19	21	AA1996	YadA homologous pe
39	19	3.2	19	21	AA1997	YadA homologous pe
40	19	3.2	1098	17	AA1998	Haemophilus adhesi
41	18	3.0	2353	17	AA1999	Haemophilus adhesi
42	18	3.0	2411	21	AA1999	Haemophilus influe
43	17	2.9	17	21	AA1999	Neisserial conserv
44	17	2.9	1094	21	AA1999	Haemophilus influe
45	16	2.7	16	21	AA1999	Neisserial conserv
46	16	2.7	16	21	AA1999	Neisserial conserv
47	15	2.5	15	21	AA1999	Neisserial conserv
48	15	2.5	15	21	AA1999	Neisserial conserv

ALIGNMENTS

RESULT 1	
AA1980	AA1980
ID	AA1980 standard; Protein; 591 AA.
XX	
AC	AA1980
XX	
DT	24-SEP-1999 (first entry)
XX	
DE	Amino acid sequence of N. meningitidis protein ORF40-1.
XX	
KW	Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW	bacterial infection; treatment.
XX	
OS	Neisseria meningitidis.
XX	
PN	WO9936544-A2.
XX	
PD	22-JUL-1999.
XX	
PF	14-JAN-1999; 99WO-IB00103.
XX	
PR	09-OCT-1998; 98GB-0022143.
PR	14-JAN-1998; 98GB-0000760.
PR	01-SEP-1998; 98GB-0019015.
XX	
PA	(CHIR-) CHIRON SPA.
XX	
PI	Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX	
DR	WPI; 1999-444400/37.
DR	N-PSDB; AAX99124.

XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
CC The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisserial  
CC bacteria, especially Neisseria meningitidis.  
XX  
SQ Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTRNHTKRASATVKTAVLATLLFAFVQASANNEQEDLYLDPVQRTVAVLIVNSDK 78  
Db |||||||  
QY 19 vseltrnhtkrasatvktavlatllfatvqasanneeqeedlyldpvqrtvavlivnsdk 78  
Db |||||||  
QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
Db |||||||  
QY 79 egtgekekeveensdwavyfnekvgvltareitlkagdnlikikngtnftyslkkdldtits 138  
QY 139 VGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
Db |||||||  
QY 139 vgteklsfsangknvnitsdtkglnfaketagtngdtvtvhlngigstltdllntgattn 198  
QY 199 VTNDNVTDDEKKRAASVKDVLNAGWNITKGVKPGTGTASDNVDFVRTYDVEFLSADTKTTT 258  
Db |||||||  
QY 199 vtndnvtddekkraasvkdvl Nagwnitkvgkpgtgtasdnvdfvrt ydtveflsadtkttt 258  
QY 259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKGENGSSTDEGGLVTAKEVIDAVN 318  
Db |||||||  
QY 259 vnveskdngkktevkigaktsvikekdgklvtgdkgensstdegeglvtakevidavn 318  
QY 319 KAGWRMKTITTANGQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
Db |||||||  
QY 319 kagwrmttttangqtgqadkfetvtsctnvtf asgkgtatvskddqgnitvmydvnvgd 378  
QY 379 ALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIINAGNNIEITRNGKNID 438  
Db |||||||  
QY 379 alnvnqlqns gwnldskavagssgkvisgnvsp skgmdetvniinagnnieitrngknid 438  
QY 439 IATSMTPQFSSVSLGAGADAPTLTSLVDGDALNVGSKDKNKPVRITNVAPGVKEGDVTNVAQ 498  
Db |||||||  
QY 439 iatsmtpqfssvslgagadap t lsvdgdalnv gskdknkpvr itnvapgvkegdvtnvaq 498  
QY 499 LKGVAQNLNNRIDNVDPGNARAGIAQAIAATAGLVQAYLPKGKSMMAIGGGTYRGEAGYAIGY 558  
Db |||||||  
QY 499 lkgvaqnl n nridnvdp gnarag iaqiaa taglvqaylp gksmmaigggtyrgeagyaigy 558  
QY 559 SSISDGGNWIKGTASGNSRGHFGASASVG YQW 591  
Db |||||||  
QY 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 2  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX

KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;

Query Match 97.0%; Score 573; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTRNHTKRASATVKTAVLATLLFAFVQASANNEQEDLYLDPVQRTVAVLIVNSDK 78  
Db |||||||  
QY 19 vseltrnhtkrasatvktavlatllfatvqasanneeqeedlyldpvqrtvavlivnsdk 78  
Db |||||||  
QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
Db |||||||  
QY 79 egtgekekeveensdwavyfnekvgvltareitlkagdnlikikngtnftyslkkdldtits 138  
QY 139 VGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
Db |||||||  
QY 139 vgteklsfsangknvnitsdtkglnfaketagtngdtvtvhlngigstltdllntgattn 198  
QY 199 VTNDNVTDDEKKRAASVKDVLNAGWNITKGVKPGTGTASDNVDFVRTYDVEFLSADTKTTT 258  
Db |||||||  
QY 199 vtndnvtddekkraasvkdvl Nagwnitkvgkpgtgtasdnvdfvrt ydtveflsadtkttt 258  
QY 259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKGENGSSTDEGGLVTAKEVIDAVN 318  
Db |||||||  
QY 259 vnveskdngkktevkigaktsvikekdgklvtgdkgensstdegeglvtakevidavn 318  
QY 319 KAGWRMKTITTANGQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
Db |||||||  
QY 319 kagwrmttttangqtgqadkfetvtsctnvtf asgkgtatvskddqgnitvmydvnvgd 378  
QY 379 ALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIINAGNNIEITRNGKNID 438  
Db |||||||  
QY 379 alnvnqlqns gwnldskavagssgkvisgnvsp skgmdetvniinagnnieitrngknid 438  
QY 439 IATSMTPQFSSVSLGAGADAPTLTSLVDGDALNVGSKDKNKPVRITNVAPGVKEGDVTNVAQ 498  
Db |||||||



Db 439 iatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvrlnvapgvkegdvtlnvaq 498

QY 499 LKGVAQNLNRRIDVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
|||||

Db 499 lkgvaqnlnnridnvdgnaragiaqaiataglvqaylpgksmmaigggtyrgeagyaigy 558

QY 559 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591  
|||||

Db 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 3

AAU06171

ID AAU06171 standard; Protein; 591 AA.

XX

AC AAU06171;

XX 24-OCT-2001 (first entry)

XX

XX N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

DE

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

KW

XX Neisseria meningitidis strain PMC21.

OS

XX

FH Key Location/Qualifiers

FT Peptide 1..51

FT /label= Signal\_peptide

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..108

FT /label= V1

FT /note= "Variable region 1"

FT Protein 52..591

FT /label= Mature\_Nhha

FT /note= "Predicted mature protein, specifically claimed in claim 12"

FT

FT Region 109..120

FT /label= C2

FT /note= "Conserved region 2"

FT Region 121..124

FT /label= V2

FT /note= "Variable region 2"

FT Region 125..188

FT /label= C3

FT /note= "Conserved region 3"

FT Region 189..210

FT /label= V3

FT /note= "Variable region 3"

FT Region 211..229

FT /label= C4

FT /note= "Conserved region 4"

FT Region 230..236

FT /label= V4

FT /note= "Variable region 4"

FT Region 237..591

FT /label= C5

FT /note= "Conserved region 5"

XX

PN WO200155182-A1.

XX

PD 02-AUG-2001.

XX

XX 25-JAN-2001; 2001WO-AU000069.

PF

XX 25-JAN-2000; 2000US-0177917.

PR

XX (UYQU ) UNIV QUEENSLAND.

PA

XX Peak IRA, Jennings MP;

PI

XX WPI; 2001-488774/53.

DR

DR N-PSDB; AAS09161.

XX

PT New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

XX

PS Claim 9; Fig 1; 9lpp; English.

XX

CC The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha

CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

XX the present invention.

SQ Sequence 591 AA;

Query Match 97.0%; Score 573; DB 22; Length 591;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNRQEEDLYLDPVQRTVAVLVNSDK 78  
|||||

Db 19 vseltrnhtkrasatvktavlatllfatvqasanneeceedlyldpvqrtvavlivnsdk 78

QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
|||||

Db 79 egtgekekveensdwavyfnekgvltareitlkagdnlkikqngtnftyslkkldtlds 138

QY 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLNTGATTN 198  
|||||

Db 139 vgteklsfsangnkvnitsdtkglnfaketagtnngdtvhlngigstltdtlnltgattn 198

QY 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTEFLSADTKTTT 258  
|||||

Db 199 vtndnvtddekkraasvkdvl nagwnikgvpkgtasdnvdfvrt ydtveflsadtkttt 258

QY 259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKGENSGSTDEGEGLVTAKEVIDAVN 318  
|||||

Db 259 vnveskdngkktevkigaktsvikekdgklvtgdkgensgstdegeglvtakevidavn 318

QY 319 KAGWRMKT TTTANGQTGQADKFETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
|||||

Db 319 kagwrmktttangqtgqadkfetvtsgtntvtfasgkgttatvskddqgnitvmydnnvgd 378

QY 379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNID 438  
|||||

Db 379 alnvnqlqns gwnlds kavagssgkvisgnvpsk gmdetvnnagnnieitrngknid 438

QY 439 IATSMTPQFSSVSLGAGADAP T LSV DGDALNVGSKDNKPVRITNVAPGVKEGDVTNVAQ 498  
|||||

Db 439 iatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvrlnvapgvkegdvtlnvaq 498

QY 499 LKGVAQNLNRRIDVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
|||||

Db 499 lkgvaqnlnnridnvdgnaragiaqaiataglvqaylpgksmmaigggtyrgeagyaigy 558

QY 559 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591  
|||||

Db 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 4

AAY23741

ID	AAV23741	standard; Protein; 591 AA.	
XX	AAV23741;		
XX	08-SEP-1999	(first entry)	
DT	A	surface protein of Neisseria meningitidis.	
XX			
DE	Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.		
XX	Neisseria meningitidis.		
OS	WO9931132-A1.		
XX	24-JUN-1999.		
PD	14-DEC-1998;	98WO-AU01031.	
XX	12-DEC-1997;	97GB-0026398.	
PF	(ISIS-)	ISIS INNOVATION LTD.	
XX	(UYQU )	UNIV QUEENSLAND.	
PA	Jennings MP,	Moxon ER, Peak IRA;	
XX	WPI; 1999-418754/35.		
DR	N-PSDB; AAX85793.		
XX	Neisseria meningitidis surface proteins useful for treating N. meningitidis infections		
PT	Claim 1;	Page 104-106; 132pp; English.	
XX	The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.		
CC	Sequence	591 AA;	
SQ	Query Match 88.8%; Score 525; DB 20; Length 591; Best Local Similarity 100.0%; Pred. No. 0; Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	67	RTVAVLIIVNSDKEGTGEKEKVEENS	DMVYFNEKGVLTFAREITLKAGDNLKIKONGTNET 126
Db			
QY	127	YSLKKDLTDLTSVGT	EKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
Db			
QY	187	TDTLNTGATNTVNDNV	TDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDT 246
Db			
QY	247	VEFLSADTKTTTVNV	SVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDKGENGSSTDEGEG 306
Db			
QY	307	LVTAKEVIDAVNKAG	WRMKTTTTANGQTGOADKFETVTSGTNTVTFASGKGTATVSKDDQG 366
Db			
QY	367	NITVMYDVNVGDAL	NVNLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNINAGN 426
Db			

Db	367	nitvmydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskqkmdetvninagn	426
QY	427	NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPFVRITNVAP	486
Db			
QY	487	GVKEGDVTNVAQLKGVAQNLNRRIDNV	DGNARAGIAQAIATAGLVQAYLPCKSMMAIGGG 546
Db			
QY	547	TYRGEAGYAIGYSSISDGGNWI	IKGTASGNSRGHFGASASVGYQW 591
Db			
QY	547	tyrgeagyaisyssisdggnwi	kgtasgnsrghfgasasvgyqw 591
XX	RESULT	5	
AAU06175	ID	AAU06175	standard; Protein; 591 AA.
XX	AC	AAU06175;	
XX	24-OCT-2001	(first entry)	
DT	N. meningitidis	EG329	surface antigen NhHA polypeptide sequence.
XX	Surface antigen NhHA;	meningococcal disease; meningitis vaccine.	
OS	Neisseria meningitidis	strain EG329.	
XX	Key	Location/Qualifiers	
FT	Region	1..50	
FT		/label= C1	
FT		/note= "Conserved region 1"	
FT	Region	51..108	
FT		/label= V1	
FT		/note= "Variable region 1"	
FT	Region	109..120	
FT		/label= C2	
FT		/note= "Conserved region 2"	
FT	Region	121..124	
FT		/label= V2	
FT		/note= "Variable region 2"	
FT	Region	125..188	
FT		/label= C3	
FT		/note= "Conserved region 3"	
FT	Region	189..210	
FT		/label= V3	
FT		/note= "Variable region 3"	
FT	Region	211..229	
FT		/label= C4	
FT		/note= "Conserved region 4"	
FT	Region	230..236	
FT		/label= V4	
FT		/note= "Variable region 4"	
FT	Region	237..591	
FT		/label= C5	
FT		/note= "Conserved region 5"	
XX	WO200155182-A1.		
PN	02-AUG-2001.		
PD	25-JAN-2001;	2001WO-AU00069.	
XX	25-JAN-2000;	2000US-0177917.	
PE	(UYQU )	UNIV QUEENSLAND.	
PR	Peak IRA,	Jennings MP;	
XX	WPI; 2001-488774/53.		
DR	N-PSDB; AAS09165.		
XX			

	New Nhha surface antigen polypeptides and polynucleotides from
	Neisseria meningitidis, useful in producing vaccines for treating or
	preventing broad spectrum of Neisseria meningitidis -
	Claim 9; Fig 1; 9lpp; English.
	The present invention relates to the isolation of novel Neisseria
	meningitidis mutant polypeptides of the surface antigen Nhha
	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
	characterised by deletions of non-conserved amino acids, particularly
	the deletion of variable regions. The deletion mutants are useful in
	diagnostics, therapeutic and prophylactic vaccines against a broader
	spectrum of N. meningitidis, and in designing and/or screening of
	medicaments. The mutant proteins when used as a vaccine can effectively
	immunise against a broader spectrum of N. meningitidis strains than
	would be expected from a corresponding wild-type surface antigen.
	The present sequence representing the wild type surface antigen Nhha
	from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
	the present invention.
	Sequence 591 AA;
	Query Match 88.8%; Score 525; DB 22; Length 591;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	67 RTVAVLIVNSDKEGTGEKEKVEENSDWAVFYNEKGVLTAAREITLKAGDNLKIKQNGTNFT 126
Db	
QY	127 YSLKKDLTLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
Db	
QY	127 yslkkdltditsvgteklsfsangknvnitsdtkglinfaketagngdtvhlngigstl 186
QY	187 TDTLLNTGATTNVNDNDVTDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDT 246
Db	
QY	187 tdtllntgattnvndnvtdekkraasvkdvlnagwnkvgkpgttasdndvdfvrttydt 246
QY	247 VEFLSADTKTTTVNESKDNGKTEVKIGAKTSVIKEKDGLVTGDKGENGSSTDEGEG 306
Db	
QY	247 veflsadtktttvnveskdngkktevkigaktsvikekdgklvtgdkgensstdegeg 306
QY	307 LVTAKEVIDAVNKAGRMTTTTANGQTGOADKFEETVTSCTNVTFASGKGTTATVSKDDQG 366
Db	
QY	307 lvtakevidavnkagrmttttangtqgadkfetvtsctnvtfasgkgttatvsksddqg 366
QY	367 NITVMYDVNVGDALNVQNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVDINAGN 426
Db	
QY	367 nitvmylvnvgdalnvqnqlnsgwnldskavagsgkvvisgnvspkskgmdetvnnagn 426
QY	427 NIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSVDGDALNVSGSKDNKPVRITNVAP 486
Db	
QY	427 gvkegdvtnvaqlkgvaqlnnrindnvdgnaragiaaiaataglvqaylpgksmmaigg 546
Db	
QY	487 TYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
Db	
QY	547 tyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 591
Db	
RESULT	6
AAU06182	ID
XX	AAU06182 standard; Protein; 512 AA.
AC	AAU06182;
XX	DT
DT	24-OCT-2001 (first entry)
XX	XX





PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 8; 9lpp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #3.  
XX  
SQ Sequence 433 AA;  
  
Query Match 64.5%; Score 381; DB 22; Length 433;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 211 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTNVNESKDNGKKT 270  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
53 raasvkdvlnagwnikgvkpgttasdnvdfvrtvdtveflsadtktttvnveskdngkkt 112  
  
QY 271 EVKIGAKTSVIKEDGKLVTKGDKGSGSSDDEGGLVTAKEVIDAVNKAGWRMKTITAN 330  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
113 evkigaktsvikekdgklvtgdkkgengsstdegeglvtakevidavnkagwrmtttan 172  
  
QY 331 GQTGOADKFETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 390  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
173 gqtgqadkfetvtsgtntvfaskgttatvskddqgnitvmydvnvgdnlvnqlnsgw 232  
  
QY 391 NLDSKAVAGSSGKVISGNVSPSKGKMDETVINAGNIEITRNGKNIDIATSMTPQFSSV 450  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
233 nldskavagsgkvisgnvspksgkmdetvinnagnnieitrngkniidiatsmtppfssv 292  
  
QY 451 SLGAGADAPTLSDGDALNVGSKKDNKPVKITNVAPGVKEGDTVNVQKGVQNLNRI 510  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
293 slgagadaptlsvgdalnvsgskdknkpvrkitnvapgvkegdtvnvqkgvqnlnnri 352  
  
QY 511 DNVDGNARAGIAQAATAGLVQAYLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIHK 570  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
353 dnvdgnaragiaqaataglvqaylpkgsmaigggtyrgeagyaigyssisdggnwiiik 412  
  
QY 571 GTASGNSRGHFGASASVGYQW 591  
Db ||||||||||||||||||||  
413 gtasgnsrghfgasasvgyqw 433  
  
RESULT 9  
AA57045  
ID AA57045 standard; Protein; 591 AA.  
XX  
AC AA57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 90  
FT /note= "Encoded by AAT"

FT Misc-difference 92 /note= "Encoded by GAT"  
FT Misc-difference 98 /note= "Encoded by AAC"  
FT Misc-difference 108 /note= "Encoded by AATC"  
FT Misc-difference 123 /note= "Encoded by ACA"  
FT Misc-difference 269 /note= "Encoded by AAA"  
FT Misc-difference 389 /note= "Encoded by CGT"  
XX  
PN WO9958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
XX N-PSDB; AAZ39865.  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BasB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 62.1%; Score 367; DB 21; Length 591;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 124 NFTYSLKKDLTLTSVGTTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIG 183  
|||  
Db 124 nftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketagtdtvtvhlngig 183  
  
QY 184 STLTDTLNLTGATNTVNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTASDNVDFVRT 243  
|||  
Db 184 stltdtllntgtatntvndnvtddkkraasvkdvl nagwnikgvkpgttasdnvdfvrt 243  
  
QY 244 YDTVEFLSADTKTTNVNESKDNGKKEVIGAKTSVIKEDGKLVTKDKGENGSSTDE 303  
|||  
Db 244 ydtveflsadtktttvtnveskdngkrtevkigaktsvikekdgklvtgdkgenssstde 303

QY 304 GEGLVTAKEVIDAVNKAGWRMKTATTANGOTGOADKFETVTSCTNVTASFSGKTTATVSKD 363  
Db 304 geglvtakevidavnkagwrmttttangtgqadkfetvtsctnvtfasgkttatvskd 363  
QY 364 DQGNITVMYDVGDNALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNN 423  
Db 364 dagnitvmydvngdlnvnlqnswnldskavagssgkvisgnvpskkgmdetvnn 423  
QY 424 AGNNIEITRNGKNIDIASTMTPOFSSVSLGAGADAPTLSDVDGDNALNVGSKKDNKPVRI 483  
Db 424 agnnieitrngknidiatsmtppfssvslgagadaptlsvdgdalnvgskkdnkpvritn 483  
QY 484 VAPGVKEGDTVNVQAQLKGVAQNLRIDNVGNARAGIAQAIATAGLVQAYLPKGKSMMAI 543  
Db 484 vapgvkegdtvnvaqlkgvaqnlrridnvdgnaragiagaiataglvqaylpgkksmmai 543  
QY 544 GGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 544 gggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 10  
AAU06184  
ID AAU06184 standard; Protein; 407 AA.  
XX AAU06184;  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 Nhha deletion mutant #2.  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.  
XX  
OS Neisseria meningitidis strain PMC21.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Protein 52..407  
FT /label= Mature\_Nhha\_deletion\_mutant\_#2  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"

XX  
PN WO200155182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
PI  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09174.  
XX  
XX New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 7; 9lpp; English.  
XX

CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #2.  
XX  
SQ Sequence 407 AA;

Query Match 60.1%; Score 355; DB 22; Length 407;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 237 NVDFVRYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGE 296  
Db 53 nvdfvrydtveflsadtktttvnveskdngkktevkigaktsvikekdgklvtgdkge 112  
QY 297 NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTATTANGOTGOADKFETVTSCTNVTASFSGKGT 356  
Db 113 ngsstdegeglvtakevidavnkagwrmttttanggtgqadkfetvtsctnvtfasgkgt 172  
QY 357 TATVSKDDQGNITVMYDVGDNALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKM 416  
Db 173 tatvskddqgnitvmydvngdlnvnlqnswnldskavagssgkvisgnvpskkgkm 232  
QY 417 DETVINAGNNIEITRNGKNIDIASTMTPOFSSVSLGAGADAPTLSDVDGDNALNVGSKKDN 476  
Db 233 detvinagnnieitrngknidiatsmtppfssvslgagadaptlsvdgdalnvgskkdn 292  
QY 477 KPVRTNVAPGVKEGDTVNVQAQLKGVAQNLRIDNVGNARAGIAQAIATAGLVQAYLP 536  
Db 293 kpvrtnvapgvkegdtvnvaqlkgvaqnlrridnvdgnaragiagaiataglvqaylp 352  
QY 537 GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 353 gksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 407

RESULT 11  
AAU06186  
ID AAU06186 standard; Protein; 502 AA.  
XX  
AC AAU06186;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 Nhha deletion mutant #4.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.  
XX  
OS Neisseria meningitidis strain PMC21.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..49  
FT /label= Signal\_peptide  
FT Protein 50..502  
FT /label= Mature\_Nhha\_deletion\_mutant\_#4  
FT /note= "Predicted mature protein, specifically  
XX claimed in claim 12"  
PN WO200155182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
PI

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XX WPI; 2001-488774/53.
DR N-PSDB; AAS09176.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 12; Fig 9; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #4.
XX
SQ Sequence 502 AA;

Query Match 60.1%; Score 355; DB 22; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 NVDFVRYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKGKLVTKDKGE 296
Db 148 nvdvfrydtveflsadtktttnvveskdngkktevkigaktsvikekdgklvtgdkge 207

QY 297 NGSSTDEGGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSGTNVTFASGKGT 356
Db 208 ngsstdegeglvtakevidavnkagwrmtttangqtgqadkfetvtsgtntvfaskgt 267

QY 357 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGM 416
Db 268 tatvskddqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskqgm 327

QY 417 DETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLTSDGALNVGSKKDN 476
Db 328 detvninagnnieitrngknidiatstmpqfssvslgagadaptltsvdalnvsgskdn 387

QY 477 KPVRIITNAPGVKEGDVTNVAQLKGVAQNLNRRIDNVNVDGNARAGIAQAIATAGLVQAYLP 536
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QY 537 GKSMMAIGGTYRGAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591
Db 448 gksmmaiggytyrgeagyaigyssisdggnwiiikgtasgnsrghfgasasvgyqw 502

RESULT 12
AAV27201
ID AAV27201 standard; Protein; 245 AA.
XX
AC AAV27201;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
OS Neisseria meningitidis.
XX
PN W09936544 -A2.
XX
PD 22-JUL-1999.
```

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XX 14-JAN-1999; 99WO-IB00103.
PF
XX 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI; 1999-444400/37.
DR N-PSDB; AAX99123.
XX
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 61; 123pp; English.
XX
CC The invention provides proteins (AAV27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 245 AA;

Query Match 29.6%; Score 175; DB 20; Length 245;
Best Local Similarity 100.0%; Pred. No. 7.7e-169;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 191 gttasdnvdfvrydtveflsadtktttnvveskdngkktevkigaktsvikekd 245

RESULT 13
AAV23740
ID AAV23740 standard; Protein; 594 AA.
XX
AC AAV23740;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
```

XX Jennings MP, Moxon ER, Peak IRA;  
PI WPI; 1999-418754/35.  
XX N-PSDB; AAX85792.  
DR Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
PT Claim 1; Page 100-101; 132pp; English.  
XX The present sequence represents a surface protein of Neisseria  
PS meningitidis which is approximately 62 kDa. The N. meningitidis  
XX surface glycoproteins, nucleic acids, the primers and optionally  
PS a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX Sequence 594 AA;  
SQ

Query Match 27.2%; Score 161; DB 20; Length 594;  
Best Local Similarity 100.0%; Pred. No. 2.9e-154;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 364 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 423  
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366 dqgnitvmydvnvgdalnvqnlqnsqwnldskavagssgkvisgnvpskkgmdetvnin 425

QY 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 464  
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ID AAY57044 standard; Protein; 594 AA.  
XX AAY57044;  
AC AAY57044;  
XX  
DT 21-FEB-2000 (first entry)  
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
XX BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 104 /note= "Encoded by AATC"  
FT  
FT  
XX WO9958683-A2.  
PN  
XX  
PD 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-EP03255.  
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XX 13-MAY-1998; 98GB-0010276.  
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XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA  
XX  
XX Ruelle J;  
PI  
XX WPI; 2000-053103/04.  
DR

DR N-PSDB; AAZ39864.  
XX  
XX New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
XX Claim 4; Fig 2; 74pp; English.  
PS  
XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing an immune  
CC polynucleotides and polypeptides are useful for generating an antibody  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 594 AA;  
Query Match 27.2%; Score 161; DB 21; Length 594;  
Best Local Similarity 100.0%; Pred. No. 2.9e-154;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 364 DQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDETVNIN 423  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
366 dqgnitvmydvnvgdalnvqnlqnsqwnldskavagssgkvisgnvpskkgmdetvnin 425

QY 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 464  
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426 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 466

RESULT 15  
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ID AAU06174 standard; Protein; 594 AA.  
XX AAU06174;  
AC AAU06174;  
XX  
DT 24-OCT-2001 (first entry)  
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
XX  
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
KW  
XX  
XX Neisseria meningitidis strain EG327.  
OS  
XX  
XX Key Location/Qualifiers  
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FT /note= "Conserved region 1"  
FT 51..104  
FT /label= V1  
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Search completed: September 5, 2002, 10:32:01  
Job time: 438 sec

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FT /label= C5  
FT /note= "Conserved region 5"

XX WO200155182-A1.

PN 02-AUG-2001.

PD 25-JAN-2001; 2001WO-AU000069.

XX 25-JAN-2000; 2000US-0177917.

PR (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

PI WPI; 2001-488774/53.

XX DR N-PSDB; AAS09164.

PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -

XX Claim 9; Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.

XX SQ Sequence 594 AA;

Query Match 27.2%; Score 161; DB 22; Length 594;  
Best Local Similarity 100.0%; Pred. No. 2.9e-154;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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306 geglvtakevidavnkagwrmktttangqtggadkffetvtsgtnvtfasgkgttatvskd 365

QY 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN 423

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

366 dqgnitvmYdvnvgdalnvNqlnsgwnldskavagssgkvvisgnvpskkgmdetvnin 425

QY 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

426 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 466

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Word size : 15

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Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	432	73.1	592	4	US-09-377-155-2
6	432	73.1	592	4	US-09-669-974-2
7	161	27.2	594	4	US-09-377-155-9
8	161	27.2	594	4	US-09-669-974-9
9	117	19.8	594	4	US-09-377-155-7
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11	117	19.8	598	4	US-09-377-155-13
12	117	19.8	598	4	US-09-669-974-13
13	116	19.6	599	4	US-09-377-155-15
14	116	19.6	599	4	US-09-669-974-15
15	103	17.4	592	4	US-09-377-155-17
16	103	17.4	592	4	US-09-669-974-17
17	93	15.7	589	4	US-09-377-155-19
18	93	15.7	589	4	US-09-669-974-19
19	93	15.7	598	4	US-09-377-155-5
20	93	15.7	598	4	US-09-669-974-5
21	19	3.2	658	1	US-09-669-995-5
22	19	3.2	658	3	US-08-685-467-5
23	19	3.2	658	4	US-08-913-942-5
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32	18	3.0	2353	4	US-09-377-155-33	Sequence 33, Appl
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ALIGNMENTS

RESULT 1  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
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; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

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Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
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; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

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Db 499 LKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
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Db 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
RESULT 3  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126  
Db 67 RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126  
QY 127 YSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTVHLNGIGISTL 186  
Db 127 YSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTVHLNGIGISTL 186  
QY 187 TDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTTASDNVDFVRYDT 246  
Db 187 TDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVPKPGTTASDNVDFVRYDT 246  
QY 247 VEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKGDKGENSGSSTDEGEG 306  
Db 247 VEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKGDKGENSGSSTDEGEG 306  
QY 307 LVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFETVTSNTVTFASGKGTTATVSKDDQ 366  
Db 307 LVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFETVTSNTVTFASGKGTTATVSKDDQ 366  
QY 367 NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNIINAGN 426  
Db 367 NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVNIINAGN 426  
QY 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPVRIITNVAP 486  
Db 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPVRIITNVAP 486  
QY 487 GYKEGDTVNVAAQLKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGG 546



Db	487	GVKEGVDVTNVAQLKGVQNLNLRIDNV DGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGG	546
Qy	547	TYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVG YQW	591
Db	547	TYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVG YQW	591

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RESULT      4
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

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Query Match		88.8%;	Score 525;	DB 4;	Length 591;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches	525;	Conservative	0;	Mismatches	0;	
				Indels	0;	
				Gaps	0;	
QY	67	RTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT	126		
Db	67	RTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT	126		
QY	127	YSLKKDLTDLTSVGT	EKLSFSAANGKVNITSDTKGLNFAKETAGTNGD	TTVHLNGIGSTL	186	
Db	127	YSLKKDLTDLTSVGT	EKLSFSAANGKVNITSDTKGLNFAKETAGTNGD	TTVHLNGIGSTL	186	
QY	187	TDTLNTGATTNVTNDNVTDDEK	KRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDT	246		
Db	187	TDTLNTGATTNVTNDNVTDDEK	KRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDT	246		
QY	247	VEFLSADTKTTTVN	VESKDNGKKTEVKIGAKTSVIKEDGKLVTKDKGENGSSTDEGE	306		
Db	247	VEFLSADTKTTTVN	VESKDNGKKTEVKIGAKTSVIKEDGKLVTKDKGENGSSTDEGE	306		
QY	307	LVTAKEVIDAVNKAGWRMKT	TTTANGQTQADKFFETVTS	GMTNVT	FASGKGTTATVSKDDQG 366	
Db	307	LVTAKEVIDAVNKAGWRMKT	TTTANGQTQADKFFETVTS	GMTNVT	FASGKGTTATVSKDDQG 366	
QY	367	NITVMYDVNVGDALNV	NQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMD	ETV	NINAGN 426	
Db	367	NITVMYDVNVGDALNV	NQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMD	ETV	NINAGN 426	
QY	427	NIEITRNGKNIDIAT	SMTPOFSSVSLGAGADAP	TL	SVGDALNVGSKKDNKPVRITNVAP 486	
Db	427	NIEITRNGKNIDIAT	SMTPOFSSVSLGAGADAP	TL	SVGDALNVGSKKDNKPVRITNVAP 486	
QY	487	GVKEGDVTNVAQLK	GAQNLNNRIDNV	DGNARAGIAQAIATAGL	VQAYLP	GKSMMAIGGG 546
Db	487	GVKEGDVTNVAQLK	GAQNLNNRIDNV	DGNARAGIAQAIATAGL	VQAYLP	GKSMMAIGGG 546
QY	547	TYRGEAGYAIGYSS	ISDGNWIIKGTASGNSRGHFGASASVGYOW	591		
Db	547	TYRGEAGYAIGYSS	ISDGNWIIKGTASGNSRGHFGASASVGYOW	591		

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RESULT      5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

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Query Match		73.1%;	Score 432;	DB 4;	Length 592;																																						
Best Local Similarity		99.8%;	Pred. NO. 0;																																								
Matches	532;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;																																						
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Db	60	DLYLDPVQRTVA	LI	VS	DK	EG	TE	KE	KE	KE	VE	NS	DW	AV	FN	EG	VT	LA	RE	IT	LK	AG	DN	LKI	119																		
QY	119	KQNGTNFTYSL	KK	DL	TD	LT	SV	GT	EK	LS	FS	AN	GN	KV	NI	TS	DT	KG	LN	FA	KE	TA	GT	AG	TT	VH	178																
Db	120	KQNGTNFTYSL	KK	DL	TD	LT	SV	GT	EK	LS	FS	AN	GN	KV	NI	TS	DT	KG	LN	FA	KE	TA	GT	AG	TT	VH	179																
QY	179	LNGIGSTLTDT	LL	NT	GAT	TN	VT	ND	NV	TD	DE	KK	RA	AS	VK	DV	LN	AG	WN	IK	GV	KP	GT	AS	DN	V	238																
Db	180	LNGIGSTLTDT	LL	NT	GAT	TN	VT	ND	NV	TD	DE	KK	RA	AS	VK	DV	LN	AG	WN	IK	GV	KP	GT	AS	DN	V	239																
QY	239	DFVRTYD	TV	EF	LS	AD	TK	TT	TV	NV	ES	KD	NG	KK	TE	VI	KE	GI	AK	TS	VI	KE	DG	KL	VT	GK	DG	ENG	298														
Db	240	DFVRTYD	TV	EF	LS	AD	TK	TT	TV	NV	ES	KD	NG	KK	TE	VI	KE	GI	AK	TS	VI	KE	DG	KL	VT	GK	DG	ENG	299														
QY	299	SSTDEGEGLV	TA	KE	VI	DA	VN	KAG	WR	MK	TTT	TAN	Q	TG	QD	AK	FET	VT	SG	TN	VT	FA	SG	KG	GT	TA	358																
Db	300	SSTDEGEGLV	TA	KE	VI	DA	VN	KAG	WR	MK	TTT	TAN	Q	TG	QD	AK	FET	VT	SG	TN	VT	FA	SG	KG	GT	TA	359																
QY	359	TVSKDDQGNIT	VM	YD	VN	VG	DAL	NV	NQ	LN	SG	WN	LD	SK	AV	GS	SG	KV	IS	GN	VS	PS	KG	KM	DE	418																	
Db	360	TVSKDDQGNIT	VM	YD	VN	VG	DAL	NV	NQ	LN	SG	WN	LD	SK	AV	GS	SG	KV	IS	GN	VS	PS	KG	KM	DE	419																	
QY	419	TVNINAGNNIE	IT	RN	GN	KNI	DI	AT	SM	TP	QF	SS	VS	LG	AG	AD	AP	TL	SV	DG	AL	NV	GS	KK	DN	KP	478																
Db	420	TVNINAGNNIE	IT	RN	GN	KNI	DI	AT	SM	TP	QF	SS	VS	LG	AG	AD	AP	TL	SV	DG	AL	NV	GS	KK	DN	KP	479																
QY	479	VRITNVP	GV	KE	GD	VT	NV	AQ	LK	GV	AQ	NL	NR	ID	NV	DG	NR	AG	IA	QA	IA	TA	GL	VQ	AY	LP	KG	538															
Db	480	VRITNVP	GV	KE	GD	VT	NV	AQ	LK	GV	AQ	NL	NR	ID	NV	DG	NR	AG	IA	QA	IA	TA	GL	VQ	AY	LP	KG	539															
QY	539	SMMAIGGGTY	R	GE	AG	Y	A	I	G	Y	S	S	I	S	D	G	G	N	W	I	I	K	G	T	A	S	G	N	R	G	H	F	G	A	S	A	S	V	G	Y	Q	W	591
Db	540	SMMAIGGGTY	R	GE	AG	Y	A	I	G	Y	S	S	I	S	D	G	G	N	W	I	I	K	G	T	A	S	G	N	R	G	H	F	G										

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application us/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 73.1%; Score 432; DB 4; Length 592;  
Best Local Similarity 99.8%; Pred. NO. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 59 DLYLDPQRTVAVLVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118  
Db 60 DLYLDPQRTVAVLVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 119  
QY 119 KONGTFTYSLKKDLTDLTSVGTKEKLSFANGKNVNITSDTKGLNFAKETAGTNGDITVH 178  
Db 120 KONGTFTYSLKKDLTDLTSVGTKEKLSFANGKNVNITSDTKGLNFAKETAGTNGDITVH 179  
QY 179 LNGIGSTLTDLTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNKIKVKGPGTTASDNV 238  
Db 180 LNGIGSTLTDLTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNKIKVKGPGTTASDNV 239  
QY 239 DFVRYDVEFLSADTKTTTVNVESKDNGKKTEYKIGAKTSVKEKDGKLVTKDKKGENG 298  
Db 240 DFVRYDVEFLSADTKTTTVNVESKDNGKKTEYKIGAKTSVKEKDGKLVTKDKKGENG 299  
QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTA 358  
Db 300 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTA 359  
QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 418  
Db 360 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 419  
QY 419 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGALNVGSKKDNKP 478  
Db 420 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGALNVGSKKDNKP 479  
QY 479 VRITNVAPGVKEGVDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP GK 538  
Db 480 VRITNVAPGVKEGVDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP GK 539  
QY 539 SMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591  
Db 540 SMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 592

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 27.2%; Score 161; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. NO. 3.5e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 304 GEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTATVSKD 363  
Db 306 GEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTATVSKD 365  
QY 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 423  
Db 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 425  
QY 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464  
Db 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 27.2%; Score 161; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. NO. 3.5e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 304 GEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTATVSKD 363  
Db 306 GEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKFFETVTSNTVTFASGKGTTATVSKD 365  
QY 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 423  
Db 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 425  
QY 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464

Db 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466

RESULT 9  
US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 19.8%; Score 117; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235  
Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 237  
QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292  
Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 294

RESULT 10  
US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 19.8%; Score 117; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235

Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 237  
QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292  
Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 294

RESULT 11  
US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 19.8%; Score 117; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235  
Db 182 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 241  
QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 292  
Db 242 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTK 298

RESULT 12  
US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 19.8%; Score 117; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.6e-102;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	176	TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS	235
Db	182	TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS	241
QY	236	DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKEVYIGAKTSVIREKDGKLVTK	292
Db	242	DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKEVYIGAKTSVIREKDGKLVTK	298

RESULT 13  
 US-09-377-155-15  
 ; Sequence 15, Application US/09377155  
 ; Patent No. 6197312  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/377, 155  
 ; CURRENT FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 15  
 ; LENGTH: 599  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-377-155-15

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Query Match          19.6%; Score 116; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	476	NKPYRITNVA	PGVKEG	DTNVAQLKGVAQN	LNRRIDNVDGNARAGTAQAIATAGLVQAYL	535
Db	484	NKPYRITNVA	PGVKEG	DTNVAQLKGVAQN	LNRRIDNVDGNARAGTAQAIATAGLVQAYL	543
QY	536	PGKSMMAIGG	TYRGEAGYAIGYSS	ISDGGNWI	IKGTASGNSRGHFGASASVGYQW	591
Db	544	PGKSMMAIGG	TYRGEAGYAIGYSS	ISDGGNWI	IKGTASGNSRGHFGASASVGYQW	599

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RESULT      14
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent NO. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599

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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

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Query Match	19.6%;	Score 116;	DB 4;	Length 599;
Best Local Similarity	100.0%;	Pred. No. 1.5e-101;		
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QY	476	NKPVRIITNVPAGYKGGDVTNVAQLKGVAQNLNRRIDTNVDGNARAGIAQAIAATAGLYQAYL	535	
db	484	NKPVRIITNVPAGYKGGDVTNVAQLKGVAQNLNRRIDTNVDGNARAGIAQAIAATAGLYQAYL	543	

	QY	536	PKSMMAIGGGTYRGEAGYAIGYSISDGGNWI	IKTASGNSRGHGFCASASVG YQW	591
	Dd	544	PKSMMAIGGGTYRGEAGYAIGYSISDGGNWI	IKTASGNSRGHGFCASASVG YQW	599

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RESULT 15
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 592

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Query Match 17.4%; Score 103; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. NO. 3e-89;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Search completed: September 5, 2002, 10:32:33  
Job time: 260 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:33:11 ; Search time 33.86 Seconds  
(without alignments)  
1677.165 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNALSALNAWAVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : ~ 15

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	2 G81133	adhesin NMB0992 [i
2	137	23.2	592	2 A81888	probable surface f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: G81133  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755  
A;Accession: G81133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-591 <TET>  
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0992

Query Match 97.0%; Score 573; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEQBEDLYLDPVQRTVAVLIVNSDK 78  
|||||  
Db 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEQBEDLYLDPVQRTVAVLIVNSDK 78  
  
QY 79 EGTGEKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
|||||  
Db 79 EGTGEKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
  
QY 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198  
|||||  
Db 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198  
  
QY 199 VTNDNVTDDKKRAASVKDVLNAGWNIKGVPGTASDNVDFVRTYDTVEFLSADTKTTT 258  
|||||  
Db 199 VTNDNVTDDKKRAASVKDVLNAGWNIKGVPGTASDNVDFVRTYDTVEFLSADTKTTT 258  
  
QY 259 VNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENSGSTDEGEGLVTAKEVIDAVN 318  
|||||  
Db 259 VNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENSGSTDEGEGLVTAKEVIDAVN 318  
  
QY 319 KAGWRMKTITANGQTGQADKFEETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
|||||  
Db 319 KAGWRMKTITANGQTGQADKFEETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
  
QY 379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRNGKNID 438  
|||||  
Db 379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRNGKNID 438  
  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNPVRITNPAPGVKEGVTNVAQ 498  
|||||  
Db 439 IATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNPVRITNPAPGVKEGVTNVAQ 498  
  
QY 499 LKGVAQNLLNRRIDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
|||||  
Db 499 LKGVAQNLLNRRIDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
  
QY 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591  
|||||  
Db 559 SSISDGGNWIKGTASGNSRGHFGASASVGYQW 591  
  
RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain z  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C;Accession: A81888  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491  
A;Reference number: A81775; MUID:20222556  
A;Accession: A81888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-592 <PAR>  
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A;Experimental source: serogroup A, strain z2491  
C;Genetics:  
A;Gene: NMA1200

Query Match 23.2%; Score 137; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.8e-131;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 294 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFEETVTSGTNVTTFASG 353  
|||||

Db 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQADKFEYVTSCTNVTFASG 353  
Qy 354 KGTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 413  
Db 354 KGTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 413  
Qy 414 GKMDETVNIAGNNIEI 430  
Db 414 GKMDETVNIAGNNIEI 430

Search completed: September 5, 2002, 10:33:11  
Job time: 208 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:39:36 ; Search time 19.19 Seconds  
(without alignments)  
1192.457 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKYRIIWNLSALNAWAVS.....TASGNSRGHFCASASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: September 5, 2002, 10:39:36  
Job time: 418 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:39:11 ; Search time 55.9 Seconds  
(without alignments)  
1828.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASASVG YQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 15

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

- Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	16	Q9JR18
2	556	94.1	591	2	Q9JPS7
3	525	88.8	591	2	Q93QY3
4	432	73.1	592	2	Q9AOF0
5	220	37.2	526	2	Q9JPS4
6	220	37.2	530	2	Q9JPS1
7	195	33.0	594	2	Q9JPI3
8	195	33.0	594	2	Q9JPS2
9	174	29.4	592	2	Q9JPS9
10	171	28.9	598	2	Q9JPR7
11	171	28.9	599	2	Q9JPS8
12	161	27.2	590	2	Q9JPS3
13	161	27.2	594	2	Q93QY4
14	137	23.2	592	16	Q9JQW4
15	117	19.8	594	2	Q9JPH7
16	117	19.8	598	2	Q9JPR9

17	117	19.8	598	2	Q9JPS0	Q9jps0 neisseria m
18	116	19.6	599	2	Q9JPR8	Q9jpr8 neisseria m
19	116	19.6	600	2	Q9JPS6	Q9jps6 neisseria m
20	116	19.6	600	2	Q9JPS5	Q9jps5 neisseria m
21	103	17.4	592	2	Q93QY2	Q93qy2 neisseria m
22	93	15.7	589	2	Q9JPI0	Q9jpi0 neisseria m
23	93	15.7	589	2	Q93QY1	Q93qy1 neisseria m
24	93	15.7	595	2	Q9JPH0	Q9jph0 neisseria m
25	93	15.7	598	2	Q9JPT0	Q9jpt0 neisseria m
26	93	15.7	598	2	Q93QY5	Q93qy5 neisseria m
27	19	3.2	1098	2	Q48152	Q48152 haemophilus
28	18	3.0	2353	2	P71401	P71401 haemophilus

ALIGNMENTS

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RESULT 1
Q9JR18
ID Q9JR18 PRELIMINARY; PRT; 591 AA.
AC Q9JR18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
DE PROTEIN).
GN GNA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Massignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AE002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -
DR EMBL; AF226370; AAF42519.1; -
DR EMBL; AF226374; AAF42523.1; -
DR EMBL; AF157611; AAK68872.1; -
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DR TIGR; NMB0992; -.  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 97.0%; Score 573; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
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Db 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
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QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
|||||  
Db 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
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QY 139 VGTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
|||||  
Db 139 VGTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
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QY 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTT 258  
|||||  
Db 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTT 258  
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QY 259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKGSGSSTDEGEGLVTAKEVIDAVN 318  
|||||  
Db 259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKGSGSSTDEGEGLVTAKEVIDAVN 318  
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QY 319 KAGWRMKT TTTANGQTGQADKFETVTSGTNVT FASGKGTATVSKDDQGNITVMYDVNVGD 378  
|||||  
Db 319 KAGWRMKT TTTANGQTGQADKFETVTSGTNVT FASGKGTATVSKDDQGNITVMYDVNVGD 378  
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QY 379 ALNVNQLQNSGNWLD SKAVAGSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNID 438  
|||||  
Db 379 ALNVNQLQNSGNWLD SKAVAGSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNID 438  
|||||

QY 439 IATSMTPQFSSVSLGACADAPTL SVGDALNVGSKKDNKPVRTITN VAPGVKEGDTVNAQ 498  
|||||  
Db 439 IATSMTPQFSSVSLGACADAPTL SVGDALNVGSKKDNKPVRTITN VAPGVKEGDTVNAQ 498  
|||||

QY 499 LKGV AQNLNRRIDNV DGNARAGIAQAIATAGLVQAYLP GKSMMAIGGGTYRGEAGYAIGY 558  
|||||  
Db 499 LKGV AQNLNRRIDNV DGNARAGIAQAIATAGLVQAYLP GKSMMAIGGGTYRGEAGYAIGY 558  
|||||

QY 559 SSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591  
|||||  
Db 559 SSISDGGNWIITKGTASGNSRGHFGASASVGYQW 591  
|||||

RESULT 2  
Q9JPS7 PRELIMINARY; PRT; 591 AA.

AC Q9JPS7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.

RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing."  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226366; AAF42515.1; -.  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAB5A91E1F CRC64;

Query Match 94.1%; Score 556; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDKETGEKEKVEENSDWAV 95  
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Db 36 TAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDKETGEKEKVEENSDWAV 95  
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QY 96 YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVYTEKLSFSANGKNVNI 155  
|||||  
Db 96 YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVYTEKLSFSANGKNVNI 155  
|||||

QY 156 TS DTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDEKKRAASV 215  
|||||  
Db 156 TS DTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDEKKRAASV 215  
|||||

QY 216 KDVLNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIG 275  
|||||  
Db 216 KDVLNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIG 275  
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QY 276 AKTSVIKEKDGKLVTKDKGSGSSTDEGEGLVTAKEVIDAVNKAGWRMKT TTTANGQTGQ 335  
|||||  
Db 276 AKTSVIKEKDGKLVTKDKGSGSSTDEGEGLVTAKEVIDAVNKAGWRMKT TTTANGQTGQ 335  
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QY 336 ADKFETVTSGTNVT FASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGNWLD SK 395  
|||||  
Db 336 ADKFETVTSGTNVT FASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGNWLD SK 395  
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QY 396 AVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSVSLGAG 455  
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Db 396 AVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSVSLGAG 455  
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QY 456 ADAPTL SVGDALNVGSKKDNKPVRTITN VAPGVKEGDTVNAQLKGVAQNLRIDNV DVG 515  
|||||  
Db 456 ADAPTL SVGDALNVGSKKDNKPVRTITN VAPGVKEGDTVNAQLKGVAQNLRIDNV DVG 515  
|||||

QY 516 NARAGIAQAIATAGLVQAYLP GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASG 575  
|||||  
Db 516 NARAGIAQAIATAGLVQAYLP GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASG 575  
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QY 576 NSRGHFGASASVGYQW 591  
|||||  
Db 576 NSRGHFGASASVGYQW 591  
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RESULT 3  
Q93QY3

AC Q93QY3 PRELIMINARY; PRT; 591 AA.  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157606; AAK68867.1; -.  
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;



Query Match		88.8%;	Score 525;	DB 2;	Length 591;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 525;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	67	RTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNT	126	
Db					
Db	67	RTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNT	126	
QY	127	YSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD	TTVHLNGIGSTL	186	
Db					
QY	187	TDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNVDFVRTYDT	246		
Db					
QY	247	VEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVIKEKDGKLVTKDKGSGSSTDEGEG	306		
Db					
QY	307	LVTAKEVIDAVNKAGWRMKT	TTTANGQTQADKFETVTS	GTNVTFASGKGTATVSKDDQG	366
Db					
QY	367	NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD	ETVNNINAGN	426	
Db					
QY	427	NIEITRNGKNIDIAT	SMTPOFSSVSLGAGADAPT	LSVDGALNVGSKKDNKPVRITNVAP	486
Db					
QY	487	GVKEGDTVNAQLKGVAQN	LNNRIDNV	DGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG	546
Db					
QY	547	TYRGEAGYAIGYSSISDGGN	WIIKGTASGNSRGHFGASASVGYQW	591	
Db					
RESULT 4					
Q9AQF0					
ID	Q9AQF0	PRELIMINARY;	PRT;	592 AA.	
AC	Q9AQF0;				
DT	01-JUN-2001	(TReMBLrel. 17, Created)			
DT	01-JUN-2001	(TReMBLrel. 17, Last sequence update)			
DT	01-JUN-2001	(TReMBLrel. 17, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN.				
GN	NHHA.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MC58;				
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;				
RT	"Identification and characterisation of a gene encoding a novel outer				
RT	membrane protein of Neisseria meningitidis.";				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF125375; AAK09243.1; -.				
SQ	SEQUENCE	592 AA;	62290 MW;	168986A97381EFC5	CRC64;

Query Match		73.1%;	Score 432;	DB 2;	Length 592;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 532;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	59	DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKI	118	
Db					
Db	60	DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENS	DWAVYFNEKGVLTAREITLKAGDNLKI	119	

QY	119	KQNGTNTFYSLKKDLTDL	TSVGTEKLSF	SANGNKVNITSDTKGLNFAKETAGTNGD	TTVH	178
Db						
Db	120	KQNGTNTFYSLKKDLTDL	TSVGTEKLSF	SANGNKVNITSDTKGLNFAKETAGTNGD	TTVH	179
QY	179	LNGIGSTLTD	LLNTGATTNTVNDNVTDD	DEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV	238	
Db						
Db	180	LNGIGSTLTD	LLNTGATTNTVNDNVTDD	DEKKRAASVKDVLNAGWNIKGVPKPGTTASDNV	239	
QY	239	DFVRTYD	TVFEFLSADTKTTTVN	VESKDKKTEVKIGAKTSVIKEKDGKLV	TGDKGKENG	298
Db						
Db	240	DFVRTYD	TVFEFLSADTKTTTVN	VESKDKKTEVKIGAKTSVIKEKDGKLV	TGDKGKENG	299
QY	299	SSTDEGEGLV	TAKEVIDAVNKAGWRMKT	TTTANGQTQADKFETVTS	GTNVTFASGKGTTA	358
Db						
Db	300	SSTDEGEGLV	TAKEVIDAVNKAGWRMKT	TTTANGQTQADKFETVTS	GTNVTFASGKGTTA	359
QY	359	TVSKDDQGNITVMYDV	NVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	MDE	418	
Db						
Db	360	TVSKDDQGNITVMYDV	NVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	MDE	419	
QY	419	TVNINAGNNIEITRNGK	NIDIATSMTPQFSSVSLGAGADAP	TLSDVDGALNVGSKKDNKP	478	
Db						
Db	420	TVNINAGNNIEITRNGK	NIDIATSMTPQFSSVSLGAGADAP	TLSDVDGALNVGSKKDNKP	479	
QY	479	VRITNVAPGVKEG	DVTNVAQLKGVAQN	LNNRIDNV	DGNARAGIAQAIATAGLVQAYLPGK	538
Db						
Db	480	VRITNVAPGVKEG	DVTNVAQLKGVAQN	LNNRIDNV	DGNARAGIAQAIATAGLVQAYLPGK	539
QY	539	SMMAIGGGTYRGEAGYA	IGYSSISDGGNWI	IKGTASGNSRGHFGASASVGYQW	591	
Db						
Db	540	SMMAIGGGTYRGEAGYA	IGYSSISDGGNWI	IKGTASGNSRGHFGASASVGYQW	592	

Query Match		37.2%;	Score 220;	DB 2;	Length 526;
Best Local Similarity		100.0%;	Pred. No. 2.3e-203;		
Matches 220;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	372	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD	ETVNNINAGNNIEIT	431	
Db	307	YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD	ETVNNINAGNNIEIT	366	
Qy	432	RNGKNIDIATSMTPQFSSVSLGAGADAP	TLSDVDGALNVGSKKDNKPVRITNVAPGVKEG	491	

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Db 367 RRGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDNKPKVRITNVAPGVKEG 426
Qy 492 DVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGE 551
Db 427 DVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGE 486
Qy 552 AGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591
Db 487 AGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 526

RESULT 6
Q9JPS1 PRELIMINARY; PRT; 530 AA.
AC Q9JPS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR EMBL; AF226369; AAF42518.1; -.
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;
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Query Match 37.2%; Score 220; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.3e-203; Indels 0; Gaps 0;
Matches 220; Conservative 0; Mismatches 0;

Qy 372 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431
Db 311 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 370
Qy 432 RRGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDNKPKVRITNVAPGVKEG 491
Db 371 RRGKNDIATSMTPQFSSVSLGAGADAPTLSDGDLNVGSKDNKPKVRITNVAPGVKEG 430
Qy 492 DVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGE 551
Db 431 DVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGE 490
Qy 552 AGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591
Db 491 AGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 530

RESULT 7
Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
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OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR EMBL; AF226369; AAF42518.1; -.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 33.0%; Score 195; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.3e-179; Indels 0; Gaps 0;
Matches 195; Conservative 0; Mismatches 0;

Qy 152 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATNTVNDNVTDDEKKR 211
Db 154 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATNTVNDNVTDDEKKR 213
Qy 212 AASVKDVLNAGWNKGVKPGTASDNVDFVRYTDTVEFLSADTKTTVNVESKDNKKTE 271
Db 214 AASVKDVLNAGWNKGVKPGTASDNVDFVRYTDTVEFLSADTKTTVNVESKDNKKTE 273
Qy 272 VKIGAKTSVIKEKDKLVTKDKGENSGSSTDEGGLVTAKEVIDAVNKAGWRMKTITANG 331
Db 274 VKIGAKTSVIKEKDKLVTKDKGENSGSSTDEGGLVTAKEVIDAVNKAGWRMKTITANG 333
Qy 332 QTGOADKFFETVTSGT 346
Db 334 QTGOADKFFETVTSGT 348

RESULT 8
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AC Q9JPS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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Query Match 33.0%; Score 195; DB 2; Length 594;











Thu Sep 5 14:36:05 2002

us-09-700-293-4.oligo.rspt

Page 8

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:40:42 ; Search time 58.74 Seconds  
(without alignments)  
1117.545 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGYQW 591

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 20

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_032802:\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	97.0	591	20	AAY27202 Amino acid sequenc
2	573	97.0	591	20	AAY23746 A surface protein
3	573	97.0	591	22	AAU06171 N. meningitidis PM
4	525	88.8	591	20	AAY23741 A surface protein
5	525	88.8	591	22	AAU06175 N. meningitidis EG
6	458	77.5	512	22	AAU06182 N. meningitidis PM
7	432	73.1	592	20	AAY23737 A surface protein
8	381	64.5	433	22	AAU06185 N. meningitidis PM
9	367	62.1	591	21	AAY57045 BASB029 amino acid
10	355	60.1	407	22	AAU06184 N. meningitidis PM
11	355	60.1	502	22	AAU06186 N. meningitidis PM

12	175	29.6	245	20	AAY27201 Amino acid sequenc
13	161	27.2	594	20	AAY23740 A surface protein
14	161	27.2	594	21	AAY57044 BASB029 amino acid
15	161	27.2	594	22	AAU06174 N. meningitidis EG
16	137	23.2	592	20	AAY27203 Amino acid sequenc
17	137	23.2	592	22	AAU06180 N. meningitidis Z2
18	117	19.8	594	20	AAY23739 A surface protein
19	117	19.8	594	22	AAU06179 N. meningitidis BZ
20	117	19.8	598	20	AAY23742 A surface protein
21	117	19.8	598	22	AAU06177 N. meningitidis H1
22	116	19.6	116	21	AAB37832 Neisserial conserv
23	116	19.6	599	20	AAY23743 A surface protein
24	116	19.6	599	22	AAU06176 N. meningitidis H3
25	103	17.4	513	22	AAU06183 N. meningitidis H4
26	103	17.4	592	20	AAY23744 A surface protein
27	103	17.4	592	22	AAU06172 N. meningitidis H4
28	93	15.7	589	20	AAY23745 A surface protein
29	93	15.7	589	22	AAU06173 N. meningitidis P2
30	93	15.7	598	20	AAY23738 A surface protein
31	93	15.7	598	22	AAU06178 N. meningitidis BZ
32	72	12.2	72	21	AAB37830 Neisserial conserv
33	59	10.0	604	22	AAU06181 N. meningitidis su
34	56	9.5	56	21	AAB37827 Neisserial conserv
35	53	9.0	53	21	AAB37828 Neisserial conserv
36	23	3.9	23	21	AAB37824 Neisserial conserv
37	20	3.4	20	21	AAB37831 Neisserial conserv

ALIGNMENTS

RESULT 1  
AAY27202  
ID AAY27202 standard; Protein; 591 AA.  
XX AAY27202;  
XX 24-SEP-1999 (first entry)  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX Neisseria meningitidis.  
XX WO9936544-A2.  
XX 22-JUL-1999.  
XX 14-JAN-1999; 99WO-IB00103.  
XX 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX (CHIR-) CHIRON SPA.  
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
XX WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX Claim 1; Page 62; 123pp; English.  
XX The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a





RESULT 3  
AAU06171  
ID AAU06171 standard; Protein; 591 AA.  
XX  
AC AAU06171;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain PMC21.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Region 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT Region 51..108  
FT /label= V1  
FT /note= "Variable region 1"  
FT Protein 52..591  
FT /label= Mature\_Nhha  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"  
FT Region 109..120  
FT /label= C2  
FT /note= "Conserved region 2"  
FT Region 121..124  
FT /label= V2  
FT /note= "Variable region 2"  
FT Region 125..188  
FT /label= C3  
FT /note= "Conserved region 3"  
FT Region 189..210  
FT /label= V3  
FT /note= "Variable region 3"  
FT Region 211..229  
FT /label= C4  
FT /note= "Conserved region 4"  
FT Region 230..236  
FT /label= V4  
FT /note= "Variable region 4"  
FT Region 237..591  
FT /label= C5  
FT /note= "Conserved region 5"  
XX  
PN WO200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PE 25-JAN-2001; 2001WO-AU000069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI; 2001-488774/53.  
DR N-PSDB; AAS09161.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 591 AA;  
  
Query Match 97.0%; Score 573; DB 22; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 19 VSELRNHTKRASATVKTAVLATLLFATVQASANNEQEEDLYLDPVQRTVAVLIVNSDK 78  
Db |||||  
QY 19 vseltrnhtkrasatvktavlatllfatvqasanneeceedlyldpvqrtvavlivnsdk 78  
Db |||||  
QY 79 EGTGEKEKVEENSDWAYVFNEKGVLTAREITLKGADNLKIKQNGTNFTYSLKKDLTDLTS 138  
Db |||||  
QY 79 egtgekekeveensdwayvfnekgvltareitlkagdnlkikqngtnftyslkkdltdlts 138  
Db |||||  
QY 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198  
Db |||||  
QY 139 vgteklsfsangnkvnitstdtkglnfaketagtnngdttvhlngigstltdtllntgattn 198  
Db |||||  
QY 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTEFLSADTKTTT 258  
Db |||||  
QY 199 vtndnvtdekkraasvkdvl nagwnikgkpgttasdnvdfvrt ydtveflsadtkttt 258  
Db |||||  
QY 259 VNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENGSSTDEGEGLVTAKEVIDAVN 318  
Db |||||  
QY 259 vnveskdngkktevkigaktsvikekdgklvtgdkgensstdegeglvtakevidavn 318  
Db |||||  
QY 319 KAGWRMKTITTANGQTGQADKFFETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD 378  
Db |||||  
QY 319 kagwrmktttangqtgqadkfetvtsgtntvfaskgttatvskddqgnitvm ydvnvgd 378  
Db |||||  
QY 379 ALNVNQLQNSGWNLDSKAVAGSSCKVISGNVSPSKCKMDETVMINAGNNIEITRNGKNID 438  
Db |||||  
QY 379 alnvnqlqns gwnldskavagssgkvisgnvspskgkmdetvminagnnieitrngknid 438  
Db |||||  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPVRIITNVAPGKEGDVTNVAQ 498  
Db |||||  
QY 439 iatsmtpqfssvslgagadap t lsvdgdalnv gskkdnkpvritnvapgk egdvt nvaq 498  
Db |||||  
QY 499 LKGVAQNLRNLRIDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Db |||||  
QY 499 lkgvaqnlnrnr idnvdgnarag iaqaiataglvqaylpgk smmaigg gtyrgeag yaigy 558  
Db |||||  
QY 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db |||||  
QY 559 ssisdggnwiikgtasgnsrghfgasasvgyqw 591  
Db |||||  
  
RESULT 4  
AAU23741  
ID AAU23741 standard; Protein; 591 AA.  
XX  
AC AAU23741;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX





QY 554 YATGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 591  
|||||  
Db 475 yaigyssisdggnwiikgtasgnsrghfgasasvgyqw 512

RESULT 7  
AAU06185  
ID AAY23737 standard; Protein; 592 AA.  
XX  
AC AAY23737;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85788.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 86-87; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 592 AA;

Query Match 73.1%; Score 432; DB 20; Length 592;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 DLYLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118  
|||||  
Db 60 dlyldpvqrtvavlivnsdkegtgekekeveensdwavfnekgvltareitlkagdnlki 119

QY 119 KONGTNFTYSLKKDLTDLTSVGTETKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTHV 178  
|||||  
Db 120 kqngtnftyslkkdldtltsvgtetklsfsangknvnitsdtkglnfaketagngdttvh 179

QY 179 LNGIGSTLTDTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNV 238  
|||||  
Db 180 lngigstltdtlntgattnvtndvtddekraasvkdvlnagwnikgvkpgttasdnv 239

QY 239 DFVRTYDTVEFLSADTKTTTTNVVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGKENG 298  
|||||

Db 240 dfvrtydtveflsadtkttttnveskdngkkktevkvktsvikekdgklvtgdkdgeng 299

QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFFETVTSGTNVTTFASGKTGA 358  
|||||  
Db 300 sstdegeglvtakevidavnkagwrmttttangtgqadkfetvtsgtntvtfasgkggta 359

QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 418  
|||||  
Db 360 tvskddqgnitvmydvnvgdalnvvnqlqnsqwnldskavagsgkvisgnvspskgkmd 419

QY 419 TVNINACNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 478  
|||||  
Db 420 tvninagnnieitrngknidiatsmtpqfssvslgagadaptsvdgdalnvsgskkdnkp 479

QY 479 VRITNVAPGVKEGDTVNTVAQLKGVAQNLNNRIDNVNVDGNARAGIAQAIATAGLVQAYLP 538  
|||||  
Db 480 vritnvapgvkegdvtnvaqlkgvaqnlnrldnvvdgnaragiaqaiataglvqaylpgk 539

QY 539 SMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
|||||  
Db 540 smmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 592

RESULT 8  
AAU06185  
ID AAU06185 standard; Protein; 433 AA.  
XX  
AC AAU06185;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 Nhha deletion mutant #3.  
DE N. meningitidis PMC21 Nhha deletion mutant #3.  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KW mutant; mutein.  
XX  
OS Neisseria meningitidis strain PMC21.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Protein 52..433  
FT /label= Mature\_Nhha\_deletion\_mutant\_#3  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"  
XX  
PN WO200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU000069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI; 2001-488774/53.  
DR N-PSDB; AAS09175.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 8; 9lpp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in



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CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #3.
XX
SQ Sequence 433 AA;

Query Match      64.5%; Score 381; DB 22; Length 433;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 RAASVKDVLNAGWNITGVKPGGTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNGKKKT 270
    |||
Db 53 raasvkdvl nagwnitg vkgpggttasdnvdfvrt ydveflsadtktttvnveskdngkkt 112

QY 271 EVKIGAKTSVIKEKDGKLVTKGDKGENGSSTDEGGLVTAKEVIDAVNKA GWRMKTTTAN 330
    |||
Db 113 evkigaktsvikekdglvtgkdkgensstdegeglvtakevidavnkagwrmktttan 172

QY 331 GQTGQADKFETVTCGNVTFEASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGW 390
    |||
Db 173 gqtgqadkfetvsgntvtfasgkgttatvskddqgnitvmydvnvgdalnv nqlqns gw 232

QY 391 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEITRNGKNIDIA TSMTPQFSSV 450
    |||
Db 233 nl dskavagssgkv isgnv spskgmdetvnnagnnieitrngknidiat smtpqfssv 292

QY 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVRITNVAPGVKEGDTVNTVAQLKGVAQN LNNRI 510
    |||
Db 293 slgagadap t lsvdgalnv gskkdnkpvr itnvapgvkegdvtnvaqlkgvaqn lnnri 352

QY 511 DNVDGNARAGIAQAIA TAGLVQAYLP GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI I 570
    |||
Db 353 dnvdgnarag iaqaiataglvqaylp gksmmaigggtyrgeag yaigyssi sdggnwi i 412

QY 571 GTASGNSRGHFGASASVGYQW 591
    |||
Db 413 gtasgnsrghfgasasvgyqw 433

RESULT 9
AAY57045
ID AAY57045 standard; Protein; 591 AA.
XX
AC AAY57045;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389
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FT /note= "Encoded by CGT"
XX
PN WO9958683-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-053103/04.
DR N-PSDB; AA239865.
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal -
XX
PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Nisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-Z39865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing an immune
CC polynucleotides and polypeptides are useful for generating an antibody
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 591 AA;
```

```
Query Match      62.1%; Score 367; DB 21; Length 591;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 124 NFTYSLKKDLTDLTSVGT EKL SFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIG 183
    |||
Db 124 nftyslkkdl tdltsvgt ekl sfsangnkvnit sdtkglnfaketag tngdttvh lngig 183

QY 184 STLTDTLLNTGATTNVNDNVTDDEKKRAASVRDVLNAGWNIKGVKPGTTASDNVDFVRT 243
    |||
Db 184 stltdtllntg attnvtndnvtdd ekkraasvkdvl nagwnikgvkpgttasdnvdfvrt 243

QY 244 YDTVEFLSADTKTTTVN VESKDNGKKTEVKIGAKTSVIKEKDGKLVTKDKKGENGSTDE 303
    |||
Db 244 ydtveflsad tktttvn veskdngkktevki gaktsvikekdglvtgdkkgengsstde 303

QY 304 GEGLVTAKEVIDAVNKA GWRMKTTTANGOTGOADKFETVTSGTNTVTFASGKGTTATVSKD 363
    |||
Db 304 geglvtakevi davnkagwrmktttangotg oadkfetvtsgtntvtfasgkgttatvskd 363

QY 364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNIN 423
    |||
Db 364 dqgnitvmyd vnvvgdalnv nqlqns gwnldskavagssgkv isgnv spskgmdetvnnin 423

QY 424 AGNNIEITRNGKNIDIA TSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRITN 483
    |||
Db 424 agnnieitrng knidiat smtpqfssvslg agadap t lsvdgalnv gskkdnkpvr itn 483
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QY	484	VAPGVKEGDTVNVAAQLKGVAAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAI	543
Db	484	vapgvkegdvtnvvaqlkgvaqnlrridnvdgnaragiaqaiataglvqaylpgksmmal	543
QY	544	GGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591
Db	544	gggtyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw	591
RESULT 10			
AAU06184			
ID	AAU06184	standard; Protein; 407 AA.	
XX	AAU06184;		
DT	24-OCT-2001	(first entry)	
DE	N. meningitidis PMC21 Nhha deletion mutant #2.		
XX			
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;		
KW	mutant; mutein.		
XX			
OS	Neisseria meningitidis strain PMC21.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..51	
FT		/label= Signal_peptide	
FT	Protein	52..407	
FT		/label= Mature_Nhha_deletion_mutant_#2	
FT		/note= "Predicted mature protein, specifically	
FT		claimed in claim 12"	
XX			
PN	WO200155182-A1.		
XX			
PD	02-AUG-2001.		
XX			
PF	25-JAN-2001; 2001WO-AU000069.		
XX			
PR	25-JAN-2000; 2000US-0177917.		
XX			
PA	(UYQU ) UNIV QUEENSLAND.		
XX			
PI	Peak IRA, Jennings MP;		
XX			
DR	WPI; 2001-488774/53.		
DR	N-PSDB; AAS09174.		
XX			
PT	New Nhha surface antigen polypeptides and polynucleotides from		
PT	Neisseria meningitidis, useful in producing vaccines for treating or		
PT	preventing broad spectrum of Neisseria meningitidis -		
XX			
PS	Claim 12; Fig 7; 9lpp; English.		
XX			
CC	The present invention relates to the isolation of novel Neisseria		
CC	meningitidis mutant polypeptides of the surface antigen Nhha		
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are		
CC	characterised by deletions of non-conserved amino acids, particularly		
CC	the deletion of variable regions. The deletion mutants are useful in		
CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
CC	spectrum of N. meningitidis, and in designing and/or screening of		
CC	medicaments. The mutant proteins when used as a vaccine can effectively		
CC	immunise against a broader spectrum of N. meningitidis strains than		
CC	would be expected from a corresponding wild-type surface antigen.		
CC	The present sequence represents N. meningitidis strain PMC21 surface		
XX	antigen Nhha deletion mutant #2.		
SQ	Sequence	407 AA;	

Query Match 60.1%; Score 355; DB 22; Length 407;  
Best Local Similarity 100.0%; Pred. No. 0;

		Matches	355;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	237	NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGDKDGE	296								
Db	53	nvdvfrtydtveflsadtktttvnveskdngkktevkigaktsvikekdglvtgkdkg	112								
QY	297	NGSSTDEGEGLVTAKEVIDAVNKAGWRMKT TTTANGQTQADKFFETVTSNTVFASGKGT	356								
Db	113	ngsstdegeglvtakevidavnkagwrmkttttangqtgqadkfetvtsntvtfasgkgt	172								
QY	357	TATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLNDSKAVAGSSGKVISGNVSPSKGKM	416								
Db	173	tatvskddqgnitvmymdvnvvgdalnvnlqnsqwnldskavagsgkvvisgnvpskgkm	232								
QY	417	DETVNINAGNNIEITRNGKNIDLATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDN	476								
Db	233	detvninagnnieitrngknidiatsmtppqfssvslgagadaptlsvdgdalnvsgkkdn	292								
QY	477	KPVRITNVAPGVKEGDTVNVAAQLKGVAAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLP	536								
Db	293	kpvritnvapgvkegdvtnvvaqlkgvaqnlrridnvdgnaragiaqaiataglvqaylp	352								
QY	537	GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW	591								
Db	353	gksmmaigggtyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw	407								
RESULT 11											
AAU06186											
ID	AAU06186 standard; Protein; 502 AA.										
XX	AAU06186;										
DT	24-OCT-2001 (first entry)										
XX											
DE	N. meningitidis PMC21 Nhha deletion mutant #4.										
XX											
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;										
KW	mutant; mutein.										
XX											
OS	Neisseria meningitidis strain PMC21.										
OS	Synthetic.										
FH	Key	Location/Qualifiers									
FT	Peptide	1..49									
FT		/label= Signal_peptide									
FT	Protein	50..502									
FT		/label= Mature_Nhha_deletion_mutant_#4									
FT		/note= "Predicted mature protein, specifically									
FT		claimed in claim 12"									
XX	WO200155182-A1.										
XX	PN										
XX	PD										
XX	02-AUG-2001.										
XX	25-JAN-2001; 2001WO-AU000069.										
XX	25-JAN-2000; 2000US-0177917.										
XX	(UYQU ) UNIV QUEENSLAND.										
XX	PA										
PI	Peak IRA,	Jennings MP;									
XX											
DR	WPI; 2001-488774/53.										
DR	N-PSDB; AAS09176.										
XX											
PT	New Nhha surface antigen polypeptides and polynucleotides from										
PT	Neisseria meningitidis, useful in producing vaccines for treating or										
PT	preventing broad spectrum of Neisseria meningitidis -										
XX											
PS	Claim 12; Fig 9; 9lpp; English.										
XX											
CC	The present invention relates to the isolation of novel Neisseria										

New Nhha surface antigen polypeptides and polynucleotides from  
Neisseria meningitidis, useful in producing vaccines for treating or  
preventing broad spectrum of Neisseria meningitidis -

Claim 12; Fig 9; 9lpp; English.

The present invention relates to the isolation of novel Neisseria









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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:41:15 ; Search time 25.54 Seconds  
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565.212 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWN\$ALNAWAVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 20

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
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5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	573	97.0	591	4	US-09-377-155-21	Sequence 21, Appl
2	573	97.0	591	4	US-09-669-974-21	Sequence 21, Appl
3	525	88.8	591	4	US-09-377-155-11	Sequence 11, Appl
4	525	88.8	591	4	US-09-669-974-11	Sequence 11, Appl
5	432	73.1	592	4	US-09-377-155-2	Sequence 2, Appli
6	432	73.1	592	4	US-09-669-974-2	Sequence 2, Appli
7	161	27.2	594	4	US-09-377-155-9	Sequence 9, Appli
8	161	27.2	594	4	US-09-669-974-9	Sequence 9, Appli
9	117	19.8	594	4	US-09-377-155-7	Sequence 7, Appli
10	117	19.8	594	4	US-09-669-974-7	Sequence 7, Appli
11	117	19.8	598	4	US-09-377-155-13	Sequence 13, Appl
12	117	19.8	598	4	US-09-669-974-13	Sequence 13, Appl
13	116	19.6	599	4	US-09-377-155-15	Sequence 15, Appl
14	116	19.6	599	4	US-09-669-974-15	Sequence 15, Appl
15	103	17.4	592	4	US-09-377-155-17	Sequence 17, Appl
16	103	17.4	592	4	US-09-669-974-17	Sequence 17, Appl
17	93	15.7	589	4	US-09-377-155-19	Sequence 19, Appl
18	93	15.7	589	4	US-09-669-974-19	Sequence 19, Appl
19	93	15.7	598	4	US-09-377-155-5	Sequence 5, Appli
20	93	15.7	598	4	US-09-669-974-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-377-155-21

; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK	78
Db	19	VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK	78
QY	79	EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS	138
Db	79	EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS	138
QY	139	VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD'TVHLNGIGSTLTDTLLNTGATTN	198
Db	139	VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD'TVHLNGIGSTLTDTLLNTGATTN	198
QY	199	VTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNDVDFVRTYDTVEFLSADTKTTT	258
Db	199	VTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNDVDFVRTYDTVEFLSADTKTTT	258
QY	259	VNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDKGENSGSSTDEGEGLVTAKEVIDAVN	318
Db	259	VNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDKGENSGSSTDEGEGLVTAKEVIDAVN	318
QY	319	KAGWRMKT'TTANGQTGQADKPFETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD	378
Db	319	KAGWRMKT'TTANGQTGQADKPFETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGD	378
QY	379	ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDFTVNIAGNNIEITRNGKNID	438
Db	379	ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDFTVNIAGNNIEITRNGKNID	438
QY	439	IATSMTPQFSSVSLGAGADAPTL\$VDGDALNVGSKKDNKPVKITNVAPGVKEGDVTNVAQ	498
Db	439	IATSMTPQFSSVSLGAGADAPTL\$VDGDALNVGSKKDNKPVKITNVAPGVKEGDVTNVAQ	498
QY	499	LKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY	558
Db	499	LKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY	558
QY	559	SSISDGGNWI\$KGTASGNSRGHFGASASVGYQW	591
Db	559	SSISDGGNWI\$KGTASGNSRGHFGASASVGYQW	591

RESULT 2  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; US-09-669-974-21

Query Match 97.0%; Score 573; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
Db 19 VSELTNRHTRKASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
  
QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKDLTDLTS 138  
Db 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKDLTDLTS 138  
  
QY 139 VGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTTVHLNGIGSTLTDTLTNTGATTN 198  
Db 139 VGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTTVHLNGIGSTLTDTLTNTGATTN 198  
  
QY 199 VTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNVDFVRYDTVEFLSADTKTTT 258  
Db 199 VTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNVDFVRYDTVEFLSADTKTTT 258  
  
QY 259 VNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVN 318  
Db 259 VNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVN 318  
  
QY 319 KAGWRMKTTTTANGQTGOADKFEETVTSCTNVTFAASGKGTATTATVSKDDQGNITVMYDVNVGD 378  
Db 319 KAGWRMKTTTTANGQTGOADKFEETVTSCTNVTFAASGKGTATTATVSKDDQGNITVMYDVNVGD 378  
  
QY 379 ALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNID 438  
Db 379 ALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNID 438  
  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVPAGVKEGDTVNTVAQ 498  
Db 439 IATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVPAGVKEGDTVNTVAQ 498  
  
QY 499 LKGAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
Db 499 LKGAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558  
  
QY 559 SSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591  
Db 559 SSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591

RESULT 3  
US-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; US-09-377-155-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 67 RIVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126  
Db 67 RIVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126  
  
QY 127 YSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTTVHLNGIGSTL 186  
Db 127 YSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTTVHLNGIGSTL 186  
  
QY 187 TDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNVDFVRYDT 246  
Db 187 TDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPTTASDNVDFVRYDT 246  
  
QY 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGNGSGSTDEGEG 306  
Db 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGNGSGSTDEGEG 306  
  
QY 307 LVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFEETVTSCTNVTFAASGKGTATTATVSKDDQ 366  
Db 307 LVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFEETVTSCTNVTFAASGKGTATTATVSKDDQ 366  
  
QY 367 NITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGN 426  
Db 367 NITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGN 426  
  
QY 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVP 486  
Db 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVP 486  
  
QY 487 GVKEGDTVNTVAQLKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGG 546  
Db 487 GVKEGDTVNTVAQLKGVAQNLLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSMMAIGGG 546  
  
QY 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591  
Db 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 591

RESULT 4  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155



; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 88.8%; Score 525; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 67 RTVAVLIVNSDKEGTEKEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNT 126  
Db 67 RTVAVLIVNSDKEGTEKEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNT 126  
  
QY 127 YSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
Db 127 YSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186  
  
QY 187 TDTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDT 246  
Db 187 TDTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDT 246  
  
QY 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGENSSSTDEGEG 306  
Db 247 VEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGENSSSTDEGEG 306  
  
QY 307 LVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTATVSKDDQG 366  
Db 307 LVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTATVSKDDQG 366  
  
QY 367 NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNINAGN 426  
Db 367 NITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNINAGN 426  
  
QY 427 NIEITRNGKNIDIATSMPTQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVKITNVAP 486  
Db 427 NIEITRNGKNIDIATSMPTQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVKITNVAP 486  
  
QY 487 GVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG 546  
Db 487 GVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG 546  
  
QY 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 547 TYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 5  
US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2  
  
Query Match 73.1%; Score 432; DB 4; Length 592;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 59 DLYLDPVQRTVAVLIVNSDKEGTEKEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKI 118  
Db 60 DLYLDPVQRTVAVLIVNSDKEGTEKEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKI 119  
  
QY 119 KQNGTNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVH 178  
Db 120 KQNGTNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVH 179  
  
QY 179 LNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNV 238  
Db 180 LNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNV 239  
  
QY 239 DFVRTYDTEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGENG 298  
Db 240 DFVRTYDTEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGDKGENG 299  
  
QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTA 358  
Db 300 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTA 359  
  
QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD 418  
Db 360 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMD 419  
  
QY 419 TVNINAGNIEITRNGKNIDIATSMPTQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 478  
Db 420 TVNINAGNIEITRNGKNIDIATSMPTQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 479  
  
QY 479 VRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGK 538  
Db 480 VRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGK 539  
  
QY 539 SMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 540 SMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 592

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

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Query Match      73.1%;   Score 432;   DB 4;   Length 592;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 532;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY  59  DLYLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAAREITLKAGDNLKI 118
      |||||||
Db   60  DLYLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAAREITLKAGDNLKI 119
      |||||||

QY  119  KQNGNFTYSLKKDLTDLTSLVGTSLKLSFSSANGNKVNITSDTKGLNFAKETAGTNGDTTVH 178
      |||||||
Db   120  KQNGNFTYSLKKDLTDLTSLVGTSLKLSFSSANGNKVNITSDTKGLNFAKETAGTNGDTTVH 179
      |||||||

QY  179  LKIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNV 238
      |||||||
Db   180  LKIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNV 239
      |||||||

QY  239  DFVRTYDTVEFLSADTKTTTNNVESKDNGKKTEVKIGAKTSVIREKDGKLVTKGDKGENG 298
      |||||||
Db   240  DFVRTYDTVEFLSADTKTTTNNVESKDNGKKTEVKIGAKTSVIREKDGKLVTKGDKGENG 299
      |||||||

QY  299  SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKFETVTSGTNNVTFASGKGTTA 358
      |||||||
Db   300  SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKFETVTSGTNNVTFASGKGTTA 359
      |||||||

QY  359  TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 418
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Db   360  TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 419
      |||||||

QY  419  TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 478
      |||||||
Db   420  TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP 479
      |||||||

QY  479  VRITNVAPGVKEGVDTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGK 538
      |||||||
Db   480  VRITNVAPGVKEGVDTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGK 539
      |||||||

QY  539  SMMAIGGGTYRGEAGYAGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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Db   540  SMMAIGGGTYRGEAGYAGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
      |||||||

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match      27.2%;   Score 161;   DB 4;   Length 594;
Best Local Similarity 100.0%;   Pred. No. 3.5e-144;
Matches 161;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  304  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 363
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Db   306  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 365
      |||||||

QY  364  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 423
      |||||||
Db   366  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 425
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QY  424  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 464
      |||||||
Db   426  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 466
      |||||||

RESULT 9
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match      27.2%;   Score 161;   DB 4;   Length 594;
Best Local Similarity 100.0%;   Pred. No. 3.5e-144;
Matches 161;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  304  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 363
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Db   306  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 365
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QY  364  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 423
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Db   366  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 425
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QY  424  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 464
      |||||||
Db   426  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 466
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RESULT 8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match      27.2%;   Score 161;   DB 4;   Length 594;
Best Local Similarity 100.0%;   Pred. No. 3.5e-144;
Matches 161;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  304  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 363
      |||||||
Db   306  GEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNNVTFASGKGTTATVSKD 365
      |||||||

QY  364  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 423
      |||||||
Db   366  DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 425
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QY  424  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 464
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Db   426  AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVD 466
      |||||||

RESULT 9
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match
Best Local Similarity 19.8%; Score 117; DB 4; Length 594;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235
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Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 237
|
QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 292
|
Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 294
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RESULT 10
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match
Best Local Similarity 19.8%; Score 117; DB 4; Length 594;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235
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Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 237
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QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 292
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Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 294
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RESULT 11
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
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; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match
Best Local Similarity 19.8%; Score 117; DB 4; Length 598;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235
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Db 182 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 241
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QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 292
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Db 242 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 298
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RESULT 12
US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match
Best Local Similarity 19.8%; Score 117; DB 4; Length 598;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 235
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Db 182 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGTTAS 241
|

QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 292
|
Db 242 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVIKEKDKGLVTGK 298
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RESULT 13
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
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; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 19.6%; Score 116; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 1.5e-101;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 476 NKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNRRIDNVGNARAGIAQAIATAGLVQAYL 535  
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Db 484 NKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNRRIDNVGNARAGIAQAIATAGLVQAYL 543  
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QY 536 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591  
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Db 544 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 599  
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RESULT 14  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 19.6%; Score 116; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 1.5e-101;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 476 NKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNRRIDNVGNARAGIAQAIATAGLVQAYL 535  
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Db 484 NKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLLNRRIDNVGNARAGIAQAIATAGLVQAYL 543  
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QY 536 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591  
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Db 544 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 599  
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RESULT 15  
US-09-377-155-17

; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-17

Query Match 17.4%; Score 103; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3e-89;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 190 LLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEF 249  
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QY 250 LSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEDGKLVTKG 292  
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Db 250 LSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEDGKLVTKG 292  
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Job time: 263 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:41:54 ; Search time 33.9 Seconds  
(without alignments)  
1675.186 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWN\$ALNAWAVS.....TASGNSRGHFGASASVGYGQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
  
Searched: 283138 seqs, 96089334 residues  
  
Word size : 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	573	97.0	591	2	G81133	adhesin NMB0992 [i
2	137	23.2	592	2	A81888	probable surface f

ALIGNMENTS

RESULT 1  
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adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: G81133  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755  
A;Accession: G81133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-591 <TET>  
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0992

Query Match 97.0%; Score 573; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78  
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QY 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
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Db 79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138  
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QY 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
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Db 139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTN 198  
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QY 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLSADTKTTT 258  
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Db 199 VTNDNVTDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLSADTKTTT 258  
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QY 259 VNVESKDNGKKTEVKIGAKTSVKEKDGKLVTKDKGGENSGSTDEGEGLVTAKEVIDAVN 318  
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Db 259 VNVESKDNGKKTEVKIGAKTSVKEKDGKLVTKDKGGENSGSTDEGEGLVTAKEVIDAVN 318  
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QY 319 KAGWRMKTTTTANGQTGOADKFEFTVTSGTNVTTFASGKGTTATVSKDDQGNITVMYDVNVGD 378  
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Db 319 KAGWRMKTTTTANGQTGOADKFEFTVTSGTNVTTFASGKGTTATVSKDDQGNITVMYDVNVGD 378  
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QY 379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNID 438  
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Db 379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNID 438  
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QY 439 IATSMTPQPFSSVSLGAGADAPTLSDGDALNVGSKKDNKPKVRITNVAPGVKEGDVTNVAQ 498  
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Db 439 IATSMTPQPFSSVSLGAGADAPTLSDGDALNVGSKKDNKPKVRITNVAPGVKEGDVTNVAQ 498  
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QY 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYGQW 591  
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Db 559 SSISDGGNWIIGKTASGNSRGHFGASASVGYGQW 591  
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RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C;Accession: A81888  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A;Reference number: A81775; MUID:20222556  
A;Accession: A81888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-592 <PAR>  
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA1200

Query Match 23.2%; Score 137; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.8e-131;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFEFTVTSGTNVTFFASG 353  
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Db 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353  
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Db 354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQNSGNLDSKAVAGSSGKVISGNVSPSK 413  
QY 414 GKMDETVNNAGNNIEI 430  
Db 414 GKMDETVNNAGNNIEI 430

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Job time: 220 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:48:19 ; Search time 19.15 Seconds  
(without alignments)  
1194.948 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNLSALNAWVAVS.....TASGNSRGHFGASASVGQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
-----	-----	-----	-----	-----	-----

No matches found

Search completed: September 5, 2002, 10:48:19  
Job time: 420 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:47:55 ; Search time 55.95 Seconds  
(without alignments)  
1827.346 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 591  
Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHGASASVG YQW 591

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 562222 seqs, 172994929 residues  
Word size : 20  
Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	97.0	591	16 Q9JR18	Q9jr18 neisseria m
2	556	94.1	591	2 Q9JPS7	Q9jps7 neisseria m
3	525	88.8	591	2 Q93QY3	Q93qy3 neisseria m
4	432	73.1	592	2 Q9AQF0	Q9aqf0 neisseria m
5	220	37.2	526	2 Q9JPS4	Q9jps4 neisseria m
6	220	37.2	530	2 Q9JPS1	Q9jps1 neisseria m
7	195	33.0	594	2 Q9JPI3	Q9jpi3 neisseria m
8	195	33.0	594	2 Q9JPS2	Q9jps2 neisseria m
9	174	29.4	592	2 Q9JPS9	Q9jps9 neisseria m
10	171	28.9	598	2 Q9JPR7	Q9jpr7 neisseria m
11	171	28.9	599	2 Q9JPS8	Q9jps8 neisseria m
12	161	27.2	590	2 Q9JPS3	Q9jps3 neisseria m
13	161	27.2	594	2 Q93QV4	Q93qv4 neisseria m
14	137	23.2	592	16 Q9JQW4	Q9jqw4 neisseria m
15	117	19.8	594	2 Q9JPH7	Q9jph7 neisseria m
16	117	19.8	598	2 Q9JPR9	Q9jpr9 neisseria m

17	117	19.8	598	2 Q9JPS0	Q9jps0 neisseria m
18	116	19.6	599	2 Q9JPR8	Q9jpr8 neisseria m
19	116	19.6	600	2 Q9JPS6	Q9jps6 neisseria m
20	116	19.6	600	2 Q9JPS5	Q9jps5 neisseria m
21	103	17.4	592	2 Q93QY2	Q93qy2 neisseria m
22	93	15.7	589	2 Q9JPI0	Q9jpi0 neisseria m
23	93	15.7	589	2 Q93QY1	Q93qy1 neisseria m
24	93	15.7	595	2 Q9JPH0	Q9jph0 neisseria m
25	93	15.7	598	2 Q9JPT0	Q9jpt0 neisseria m
26	93	15.7	598	2 Q93QY5	Q93qy5 neisseria m

ALIGNMENTS

RESULT 1  
Q9JR18  
ID Q9JR18 PRELIMINARY; PRT; 591 AA.  
AC Q9JR18;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).  
DE GNA992 OR NMB0992 OR NHHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";  
RT Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";  
RT Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=N.meningitidis; STRAIN=PMC21;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";  
RT Submitted (JUN-1999) to the EMBL/GenBank/DBDJ databases.  
RL EMBL; AF226375; AAF42524.1; -.  
DR EMBL; AE002450; AAF41395.1; -.  
DR EMBL; AF226367; AAF42516.1; -.  
DR EMBL; AF226370; AAF42519.1; -.  
DR EMBL; AF226374; AAF42523.1; -.  
DR EMBL; AF157611; AAK68872.1; -.  
DR TIGR; NMB0992; -.  
KW Complete proteome.





Query Match		88.8%;	Score 525;	DB 2;	Length 591;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches	525;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
QY	67	RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFT	126		
Db	67	RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFT	126		
		RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFT	126		
QY	127	YSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL	186		
Db	127	YSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL	186		
		YSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL	186		
QY	187	TDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDT	246		
Db	187	TDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDT	246		
		TDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDT	246		
QY	247	VEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENGSTDEGEG	306		
Db	247	VEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENGSTDEGEG	306		
		VEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENGSTDEGEG	306		
QY	307	LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG	366		
Db	307	LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG	366		
		LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG	366		
QY	367	NITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGN	426		
Db	367	NITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGN	426		
		NITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGN	426		
QY	427	NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAP	486		
Db	427	NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAP	486		
		NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAP	486		
QY	487	GVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGG	546		
Db	487	GVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGG	546		
		GVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGG	546		
QY	547	TYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591		
Db	547	TYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591		
		TYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591		

RESULT 4	
Q9AQF0	
ID	Q9AQF0
AC	Q9AQF0;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	OUTER MEMBRANE PROTEIN.
GN	NHHA.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MC58;
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT	"Identification and characterisation of a gene encoding a novel outer
RT	membrane protein of Neisseria meningitidis.";
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF125375; AAK09243.1; -.
SQ	SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match		73.1%;	Score 432;	DB 2;	Length 592;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches	532;	Conservative	0;	Mismatches	1;
		Indels	0;	Gaps	0;
QY	59	DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKI	118		
Db	60	DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKI	119		
		DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKI	119		
QY	119	KONGTNFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVH	178		

Query Match		88.8%;	Score 525;	DB 2;	Length 591;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches	525;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
Db	120	KONGTNFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVH	179		
QY	179	LNGIGSTLTDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNV	238		
Db	180	LNGIGSTLTDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNV	239		
		LNGIGSTLTDTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPKGTASDNV	239		
QY	239	DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENG	298		
Db	240	DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENG	299		
		DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTGKDKGENG	299		
QY	299	SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA	358		
Db	300	SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA	359		
		SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA	359		
QY	359	TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDE	418		
Db	360	TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDE	419		
		TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDE	419		
QY	419	TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP	478		
Db	420	TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP	479		
		TVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKP	479		
QY	479	VRITNVAPGVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGK	538		
Db	480	VRITNVAPGVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGK	539		
		VRITNVAPGVKEGDTVNTVAQLKGVAQNLRNDRIDNVGDNARAGIAQAIATAGLVQAYLPGK	539		
QY	539	SMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	591		
Db	540	SMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	592		
		SMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW	592		

RESULT 5	
Q9JPS4	
ID	Q9JPS4
AC	Q9JPS4;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	OUTER MEMBRANE PROTEIN GNA992.
GN	GNA992.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NG6/88;
RX	MEDLINE=20175756; PubMed=10710308;
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA	Moxon E.R., Grandi G., Rappuoli R.;
RT	"Identification of Vaccine Candidates Against Serogroup B
RT	Meningococcus by Whole-Genome Sequencing.";
RL	Science 287:1816-1820(2000).
DR	EMBL; AF226377; AAF42526.1; -.
SQ	SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;

Query Match		37.2%;	Score 220;	DB 2;	Length 526;
Best Local Similarity		100.0%;	Pred. No. 2.3e-203;		
Matches	220;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
QY	372	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGNIEIT	431		
Db	307	YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGNIEIT	366		
		YDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGNIEIT	366		
QY	432	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAPGVKEG	491		
Db	367	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAPGVKEG	426		
		RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPKVRITNVAPGVKEG	426		







DR EMBL; AF226364; AAF42513.1; -. 46C2E974AF7F78E9 CRC64;
SQ SEQUENCE 599 AA; 62693 MW; 28.9%; Score 171; DB 2; Length 599;
Query Match 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 4.7e-156;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 294 KGENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVTFASG 353
Db 301 KGENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVTFASG 360
Qy 354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 413
Db 361 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Qy 414 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 464
Db 421 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 471
RESULT 12
Q9JPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI\_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -. 8AA476AC300D80C8 CRC64;
SQ SEQUENCE 590 AA; 61661 MW; 27.2%; Score 161; DB 2; Length 590;
Query Match 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 2.1e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 108 ITLKAGDNLKIKQNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVNITSTKGLNFAKE 167
Db 106 ITLKAGDNLKIKQNGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVNITSTKGLNFAKE 165
Qy 168 TAGTNGDTTTHLNGIGSTLTDLTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIK 227
Db 166 TAGTNGDTTTHLNGIGSTLTDLTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIK 225
Qy 228 VKPGTTASDNVDVFTYDVEFLSADTKTTVNVEKDNKG 268
Db 226 VKPGTTASDNVDVFTYDVEFLSADTKTTVNVEKDNKG 266
RESULT 13
Q93QY4
ID Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI\_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -. 9DDD48B04B3A8EA2 CRC64;
SQ SEQUENCE 594 AA; 62297 MW; 27.2%; Score 161; DB 2; Length 594;
Query Match 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 2.1e-146;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVTFASGKGTATVSKD 363
Db 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSNTVTFASGKGTATVSKD 365
Qy 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
Db 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
Qy 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 464
Db 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466
RESULT 14
Q9JQW4
ID Q9JQW4 PRELIMINARY; PRT; 592 AA.
AC Q9JQW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE SURFACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).
GN NMA1200 OR GNA992.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI\_TaxID=65699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=205900, BZ133, F6124, AND Z2491;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B



```
RT Meningococcus by Whole-Genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL; AL162755; CAB84461.1; -.
DR EMBL; AF226357; AAF42506.1; -.
DR EMBL; AF226365; AAF42514.1; -.
DR EMBL; AF226373; AAF42522.1; -.
DR EMBL; AF226386; AAF42535.1; -.
KW Complete proteome.
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match      23.2%; Score 137; DB 16; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-123;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTSGTVNVTFFASG 353
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Db 294 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKT TTANGQTGQADKFETVTSGTVNVTFFASG 353

QY 354 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK 413
      |||
Db 354 KGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSK 413

QY 414 GKMDETVNINAGNNIEI 430
      |||
Db 414 GKMDETVNINAGNNIEI 430

RESULT 15
Q9JPH7
ID Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RP SEQUENCE FROM N.A.
RC STRAIN=BZ198, AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ198;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226368; AAF42517.1; -.
DR EMBL; AF226358; AAF42507.1; -.
DR EMBL; AF157604; AAK68865.1; -.
SQ SEQUENCE 594 AA; 62361 MW; 436BDDDED68263C5C CRC64;

Query Match      19.8%; Score 117; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 5.8e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS 235
      |||
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```
Db 178 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS 237
QY 236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGK 292
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Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGK 294

Search completed: September 5, 2002, 10:47:57
Job time: 428 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:33:13 ; Search time 58.74 Seconds  
(without alignments)  
1123.218 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWN\$ALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 20

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594	100.0	594	20	AA1980
2	594	100.0	594	21	AA1981
3	594	100.0	594	22	AA1982
4	161	27.1	407	22	AA1983
5	161	27.1	433	22	AA1984
6	161	27.1	502	22	AA1985
7	161	27.1	512	22	AA1986
8	161	27.1	591	20	AA1987
9	161	27.1	591	20	AA1988
10	161	27.1	591	20	AA1989
11	161	27.1	591	21	AA1990

12	161	27.1	591	22	AA1991	N. meningitidis PM
13	161	27.1	591	22	AA1992	N. meningitidis EG
14	161	27.1	592	20	AA1993	A surface protein
15	138	23.2	513	22	AA1994	N. meningitidis H4
16	138	23.2	589	20	AA1995	A surface protein
17	138	23.2	589	22	AA1996	N. meningitidis P2
18	138	23.2	592	20	AA1997	A surface protein
19	138	23.2	592	22	AA1998	N. meningitidis H4
20	138	23.2	598	20	AA1999	A surface protein
21	138	23.2	598	20	AA2000	A surface protein
22	138	23.2	598	22	AA2001	N. meningitidis H1
23	138	23.2	598	22	AA2002	N. meningitidis BZ
24	127	21.4	592	20	AA2003	Amino acid sequenc
25	127	21.4	592	22	AA2004	N. meningitidis Z2
26	98	16.5	245	20	AA2005	Amino acid sequenc
27	94	15.8	599	20	AA2006	A surface protein
28	94	15.8	599	22	AA2007	N. meningitidis H3
29	93	15.7	594	20	AA2008	A surface protein
30	93	15.7	594	22	AA2009	N. meningitidis BZ
31	82	13.8	116	21	AA2010	Neisserial conserv
32	72	12.1	72	21	AA2011	Neisserial conserv
33	59	9.9	604	22	AA2012	N. meningitidis su
34	43	7.2	53	21	AA2013	Neisserial conserv
35	32	5.4	56	21	AA2014	Neisserial conserv
36	23	3.9	1098	17	AA2015	Haemophilus adhesi
37	22	3.7	2353	17	AA2016	Haemophilus influe
38	22	3.7	2411	21	AA2017	Haemophilus influe
39	20	3.4	20	21	AA2018	Neisserial conserv

ALIGNMENTS

RESULT 1  
AA1980  
ID AA1980 standard; Protein; 594 AA.  
XX  
AC AA1980;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
(UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
meningitidis infections  
XX  
PS Claim 1; Page 100-101; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
meningitidis which is approximately 62 kDa. The N. meningitidis  
surface glycoproteins, nucleic acids, the primers and optionally  
a thermostable polymerase, or antibodies are useful in a kit for

the detection or diagnosis of *N. meningitidis* infection in humans. The *N. meningitidis* surface glycoproteins can also be used to prevent or treat *N. meningitidis* infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

	Query Match	100.0%;	Score 594;	DB 20;	Length 594;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	1	mnkiyriiwns	alnawvavseltrnhtkrasatvatavlatll	llfatvgasttddddlyle 60		
QY	61	PVQRTAVVLSFR	SDKEGTGEKEVTEDSNWGVYFDKKGVL	TAGTITLKAGDNLKIKQNTNE 120		
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QY	121	NTNASSFTYS	LKKDLTDLTSVGT	EKLSFSANSKNVNITSDTKGLNFAKKTAE	TNGDTVH 180	
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QY	181	LNIGIGSTL	DTLLENTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN	IKGVKPGTTASDNV 240		
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Db	241	dfrtydtvefls	adtkttttnveskdngkrtevkigaktsvikekdglvtgdkgend 300			
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Db	301	sstdkgeglv	takevidavnkagwrmktttangqtgqadkffetvstgntvtfasgkgtta 360			
QY	361	TVSKDDQ	GNITVMYDVNVGDALNVNQLNSGWN	LDSKAVAGSSGKVISGNVSPSKGMDE 420		
Db	361	tvsdkdqqn	itvmvdydvngdalnvnqlnsgwnldskavagssgkvisgnvpskgmde 420			
QY	421	TVNINAGN	NIETRN	GNKIDIIATSMTPQFSSVSLGACADAPTLSV	DDREGALNVGSKDANK 480	
Db	421	tvninagnn	ieitrngknidiatstmpqfssvslgagadaptlsvddregalnvsgskdank 480			
QY	481	PVRITNV	APGVKEG	DVTNVAQLKGVAQN	LNNHIDNV	DGNARAGIAQAIATAGLVQAYLP 540
Db	481	pvritnvap	gvkegdvtnvvaqlkgvaqnlnnhidnvdgnaragiaqaiataglvqaylp 540			
QY	541	KSMMAIGG	GTYRGEAGYAIGYSSIS	DGGNWI	IKGTASGNSRGHFGASASVGYQW 594	
Db	541	ksmmaigg	gtyrgeagyaigyssisdggwnwikgtasgnsrghfgasasvgyqw 594			

PN W09958683-A2.  
 XX 18-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99WO-EP03255.  
 XX  
 PR 13-MAY-1998; 98GB-0010276.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Ruelle J;  
 XX  
 DR WPI; 2000-053103/04.  
 DR N-PSDB; AAZ39864.  
 XX  
 PT New polypeptide from neisseria meningitidis useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal -  
 XX  
 PS Claim 4; Fig 2; 74pp; English.  
 XX  
 CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
 CC *Haemophilus influenzae* surface fibril (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
 CC polypeptide sequences (AAZ57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 CC meningitidis infection in a mammal. Compositions containing a BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with *Neisseria*  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.  
 XX  
 SQ Sequence 594 AA;  
  
 Query Match 100.0%; Score 594; DB 21; Length 594;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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 1 mnkiyriiwnlsalnawvavseltrnhtkrasatvatatlatllfatvqasttdddddlyle 60  
  
 QY 61 PVORTAVLSFRSDKEGTGEKTEVSDSNWGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 61 pvortavlsfrsdkegtekevtsdsnwgvyfdkkgvltagtitlkagdnlkikontne 120  
  
 QY 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNPAKKTAEETNGDPTVH 180  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 121 ntnassfty slkldtldtsvgteklsfsansknvnitsdtkglnfakktaeetngdptvh 180  
  
 QY 181 LNCIGSTLTDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIGVKPGTTASDNV 240  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 181 lngigstltdtllntgattnvtndvtddekkraasvkdvl nagwnkigvkpgttasdnv 240  
  
 QY 241 DfVRTYDTVEFLSADTKTTTNNVESKDNGKRTEVKIGAKTSVIEKDGKLVTKDKGEND 300  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 241 dfvrt ydtveflsadtktttnvveskdngkrtevkigaktsviekdgklvtgdkgend 300  
  
 QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTA 360  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 301 sstdkgeglvtakevidavnkagwrmktttangqtqadkfetvtsgtntvtfasgkgtta 360  
  
 QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLONSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420



Db 361 tvskddqgnltvmydvnvgdalnvnglqnswnldskavagssgkvlsnvspkskmd 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480  
Db 421 tvninagnnieitrngknidiatsmtpqfssvslgagadaptlsvddegalnvgskdank 480  
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Db 481 pvrItnvapgvkegdvtnvvaqlkgvaqnlhnhidnvdgnaragიააიაataglvqaylpg 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 3  
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ID AAU06174 standard; Protein; 594 AA.  
XX  
AC AAU06174;

DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain EG327.

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FT /note= "Conserved region 1"  
FT Region 51..104  
FT /label= V1  
FT /note= "Variable region 1"  
FT Region 105..116  
FT /label= C2  
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FT Region 117..126  
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FT /note= "Variable region 4"  
FT Region 239..594  
FT /label= C5  
FT /note= "Conserved region 5"

XX  
PN WO200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU000069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;  
PI  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09164.

XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis; useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 9lpp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 594 AA;

Query Match 100.0%; Score 594; DB 22; Length 594;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 mnkiyriiwnalsalnawavavseltrnhtkrasatvatavlatllfatvqasttddddlyle 60  
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Db 121 ntnassfty slkkdltdltsvgtekl sfsansknvntsdtkglnfakkt aetngdttvh 180  
QY 181 LNGIGSTLTDTLLNTGATNTVNDNVTDEKKRAASVKDVLNAGWNKGVKPGTASDNV 240  
Db 181 lngigstltdtllntgattnvndnvtdekkraasvkdvlnagwnikgvkpgttasdnv 240  
QY 241 DfVRTYDTVEFLSADTKTTVNVESKDNKGRTEVKICAKTSVIKEKDGLVTGDKKGEND 300  
Db 241 dfvrt ydtveflsadtkttvnveskdngkrtevkigaktsvikekdgklvtgdkkgend 300  
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Db 301 sstdkgeglvtakevidavnkagwrmktttangq tgoadkfetvtsgtntvfaskggtta 360  
QY 361 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLD SKAVAGSSGKVISGNVSPSKGMDE 420  
Db 361 tvskddqgnitvmydvnvgdalnv nqlnsgwnldskavagssgkv isgnvpspskgmde 420  
QY 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480  
Db 421 tvninagnnieitrngknidiatsmtpqfssvslgagadap tlvdddeg alnvgskdank 480  
QY 481 PVRITNVAPGVKEGDTVNVVAQLKGVAQNLNHNHIDNVGDNARAGIAQAATAGLVQAYLPG 540  
Db 481 pvrItnvapgvkegdvtnvvaqlkgvaqnlhnhidnvdgnaragიააიაataglvqaylpg 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 4  
AAU06184  
ID AAU06184 standard; Protein; 407 AA.

```
XX AC AAU06184;
XX AC
XX DT
XX DE
XX DE 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhha deletion mutant #2.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX KW mutant; mutein.
XX OS
XX OS Neisseria meningitidis strain PMC21.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..51
XX FT /label= Signal_peptide
XX FT Protein 52..407
XX FT /label= Mature_Nhha_deletion_mutant_#2
XX FT /note= "Predicted mature protein, specifically
XX FT claimed in claim 12"
XX PN WO200155182-A1.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 25-JAN-2001; 2001WO-AU000069.
XX PR 25-JAN-2001; 2000US-0177917.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX XX
XX PI Peak IRA, Jennings MP;
XX XX WPI; 2001-488774/53.
XX DR N-PSDB; AAS09174.
XX XX
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 12; Fig 7; 91pp; English.
XX XX
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence represents N. meningitidis strain PMC21 surface
XX CC antigen Nhha deletion mutant #2.
XX XX
XX SQ Sequence 407 AA;

Query Match 27.1%; Score 161; DB 22; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTTFASGKGTATVSKD 365
Db 120 geglvtakevidavnkagwrmktttangqtgqadkfetvtsgtntvtfasgkgtatvskd 179
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425
Db 180 dqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvvisgnvspskgmdetvnin 239
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSD 466
Db 240 agnnieitrngknidiatmtppqfssvslgagadaptlsvd 280
```

```
RESULT 5
AAU06185
ID AAU06185 standard; Protein; 433 AA.
XX AC
XX AC AAU06185;
XX DT 24-OCT-2001 (first entry)
XX XX
XX DE N. meningitidis PMC21 Nhha deletion mutant #3.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX KW mutant; mutein.
XX OS
XX OS Neisseria meningitidis strain PMC21.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..51
XX FT /label= Signal_peptide
XX FT Protein 52..433
XX FT /label= Mature_Nhha_deletion_mutant_#3
XX FT /note= "Predicted mature protein, specifically
XX FT claimed in claim 12"
XX XX
XX PN WO200155182-A1.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 25-JAN-2001; 2001WO-AU000069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PR (UYQU ) UNIV QUEENSLAND.
XX XX
XX PI Peak IRA, Jennings MP;
XX XX WPI; 2001-488774/53.
XX DR N-PSDB; AAS09175.
XX XX
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 12; Fig 8; 91pp; English.
XX XX
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence represents N. meningitidis strain PMC21 surface
XX CC antigen Nhha deletion mutant #3.
XX SQ Sequence 433 AA;
```

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Query Match 27.1%; Score 161; DB 22; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTTFASGKGTATVSKD 365
Db 146 geglvtakevidavnkagwrmktttangqtgqadkfetvtsgtntvtfasgkgtatvskd 205
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425
Db 366 dqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvvisgnvspskgmdetvnin 425
```

Db	206	dqgnitvmydvngdlnvnqlnsgwnldskavagssgkvvisgnvpsksgkmdetvnn	265
QY	426	AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD	466
Db	266	agnnieitrngkniatstmpqfssvslgagadaptsvd	306
RESULT	6		
AAU06186			
ID	AAU06186	standard; Protein; 502 AA.	
XX			
AC	AAU06186;		
DT	24-OCT-2001	(first entry)	
XX			
DE	N. meningitidis PMC21	Nhha deletion mutant #4.	
XX			
KW	Surface antigen Nhha;	meningococcal disease; meningitis vaccine;	
KW	mutant; mutein.		
XX			
OS	Neisseria meningitidis strain PMC21.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..49	
FT		/label= Signal_peptide	
FT	Protein	50..502	
FT		/label= Mature_Nhha_deletion_mutant_#4	
FT		/note= "Predicted mature protein, specifically	
FT		claimed in claim 12"	
XX			
PN	WO200155182-A1.		
XX			
PD	02-AUG-2001.		
XX			
PF	25-JAN-2001; 2001WO-AU000069.		
XX			
PR	25-JAN-2000; 2000US-0177917.		
XX			
PA	(UYQU ) UNIV QUEENSLAND.		
XX			
PI	Peak IRA, Jennings MP;		
XX			
DR	WPI; 2001-488774/53.		
DR	N-PSDB; AAS09176.		
XX			
PT	New Nhha surface antigen polypeptides and polynucleotides from		
PT	Neisseria meningitidis, useful in producing vaccines for treating or		
PT	preventing broad spectrum of Neisseria meningitidis -		
XX			
PS	Claim 12; Fig 9; 91pp; English.		
XX			
CC	The present invention relates to the isolation of novel Neisseria		
CC	meningitidis mutant polypeptides of the surface antigen Nhha		
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are		
CC	characterised by deletions of non-conserved amino acids, particularly		
CC	the deletion of variable regions. The deletion mutants are useful in		
CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
CC	spectrum of N. meningitidis, and in designing and/or screening of		
CC	medicaments. The mutant proteins when used as a vaccine can effectively		
CC	immunise against a broader spectrum of N. meningitidis strains than		
CC	would be expected from a corresponding wild-type surface antigen.		
CC	The present sequence represents N. meningitidis strain PMC21 surface		
CC	antigen Nhha deletion mutant #4.		
XX			
SQ	Sequence	502 AA;	
Query Match 27.1%; Score 161; DB 22; Length 502;			
Best Local Similarity 100.0%; Pred. No. 1.3e-149;			
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	306	GEGLVTAKEVIDAVNKAGWRMKTttTANGQTGQADKFETVTSgtnvtfasgkgttatvskd	365

Db	215	geglvtakevidavnkagwrmttttangtqgqadkfetvtsgtnvtfasgkgttatvskd	274
QY	366	DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN	425
Db	275	dqgnitvmydvngdlnvnqlnsgwnldskavagssgkvvisgnvpsksgkmdetvnn	334
QY	426	AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD	466
Db	335	agnnieitrngkniatstmpqfssvslgagadaptsvd	375
RESULT	7		
AAU06182			
ID	AAU06182	standard; Protein; 512 AA.	
XX			
AC	AAU06182;		
DT	24-OCT-2001	(first entry)	
XX			
DE	N. meningitidis PMC21	Nhha deletion mutant #1.	
XX			
KW	Surface antigen Nhha;	meningococcal disease; meningitis vaccine;	
KW	mutant; mutein.		
XX			
OS	Neisseria meningitidis strain PMC21.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..51	
FT		/label= Signal_peptide	
FT	Protein	52..512	
FT		/label= Mature_Nhha_deletion_mutant_#1	
FT		/note= "Predicted mature protein, specifically	
FT		claimed in claim 12"	
XX			
PN	WO200155182-A1.		
XX			
PD	02-AUG-2001.		
XX			
PF	25-JAN-2001; 2001WO-AU000069.		
XX			
PR	25-JAN-2000; 2000US-0177917.		
XX			
PA	(UYQU ) UNIV QUEENSLAND.		
XX			
PI	Peak IRA, Jennings MP;		
XX			
DR	WPI; 2001-488774/53.		
DR	N-PSDB; AAS09172.		
XX			
PT	New Nhha surface antigen polypeptides and polynucleotides from		
PT	Neisseria meningitidis, useful in producing vaccines for treating or		
PT	preventing broad spectrum of Neisseria meningitidis -		
XX			
PS	Claim 12; Fig 5; 91pp; English.		
XX			
CC	The present invention relates to the isolation of novel Neisseria		
CC	meningitidis mutant polypeptides of the surface antigen Nhha		
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are		
CC	characterised by deletions of non-conserved amino acids, particularly		
CC	the deletion of variable regions. The deletion mutants are useful in		
CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
CC	spectrum of N. meningitidis, and in designing and/or screening of		
CC	medicaments. The mutant proteins when used as a vaccine can effectively		
CC	immunise against a broader spectrum of N. meningitidis strains than		
CC	would be expected from a corresponding wild-type surface antigen.		
CC	The present sequence represents N. meningitidis strain PMC21 surface		
CC	antigen Nhha deletion mutant #1.		
XX			
SQ	Sequence	512 AA;	

Query Match		27.1%;	Score 161;	DB 22;	Length 512;				
Best Local Similarity		100.0%;	Pred. No. 1.3e-149;						
Matches 161;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
QY	306	GEGLVTAKEVIDAVNKAGWRMKT	TTTANGQTGOADKPFETVTS	GTNVTFFASGKTTATVSKD	365				
Db	225	geglvtakevidavnkagwrmtt	tangqtgqadkfetvts	gtntvfaskgttatvskd	284				
QY	366	DQGNITVMYDVNVGDALNVNQLNSGWNLD	SKAVAGSSGKVISGNVSPSKGMD	ETVNNIN	425				
Db	285	dqgnitvmydvnvgdalnvqlnsgwnld	skavagssgkvisgnvpsk	gkmdetvnn	344				
QY	426	AGNIEITRNGKNIDIATSMTPQFSSVSLG	AGADAPTL	SVD 466					
Db	345	agnieitrngknidiatsmt	pqfssvslgagadap	tlsvd 385					
RESULT 8									
AAAY27202									
ID	AAAY27202	standard;	Protein;	591 AA.					
XX	AC								
XX	AAAY27202;								
DT	24-SEP-1999	(first entry)							
DE	Amino acid sequence of N. meningitidis protein ORF40-1.								
XX									
KW	Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;								
KW	bacterial infection; treatment.								
XX									
OS	Neisseria meningitidis.								
XX									
PN	WO9936544-A2.								
XX									
PD	22-JUL-1999.								
XX									
PF	14-JAN-1999;	99WO-IB00103.							
XX									
PR	09-OCT-1998;	98GB-0022143.							
PR	14-JAN-1998;	98GB-0000760.							
PR	01-SEP-1998;	98GB-0019015.							
XX									
PA	(CHIR-) CHIRON SPA.								
XX									
PI	Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;								
XX									
DR	WPI; 1999-444400/37.								
DR	N-PSDB; AAX99124.								
XX									
PT	New protein and its nucleotide sequence, useful in vaccines or								
PT	diagnostic compositions for treating and/or preventing Neisseria								
PT	meningitidis infections								
XX									
PS	Claim 1; Page 62; 123pp; English.								
XX									
CC	The invention provides proteins (AAAY27201-245) from Neisseria								
CC	meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)								
CC	encoding the proteins. Compositions comprising the protein, nucleic acid								
CC	or antibody specific to the protein are useful as pharmaceuticals, e.g. a								
CC	vaccine composition or a diagnostic composition. The composition is also								
CC	useful for treating or preventing an infection due to Neisserial								
CC	bacteria, especially Neisseria meningitidis.								
XX									
SQ	Sequence	591 AA;							
Query Match									
Best Local Similarity		27.1%;	Score 161;	DB 20;	Length 591;				
Matches 161;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
QY	306	GEGLVTAKEVIDAVNKAGWRMKT	TTTANGQTGOADKPFETVTS	GTNVTFFASGKTTATVSKD	365				
Db	304	geglvtakevidavnkagwrmtt	tangqtgqadkfetvts	gtntvfaskgttatvskd	363				

QY	366	DQGNITVMYDVNVGDALNVNQLNSGWNLD	SKAVAGSSGKVISGNVSPSKGMD	ETVNNIN	425
Db	364	dqgnitvmydvnvgdalnvqnsgwnld	skavagssgkvisgnvpsk	gkmdetvnn	423
QY	426	AGNIEITRNGKNIDIATSMTPQFSSVSLG	AGADAPTL	SVD	466
Db	424	agnieitrngknidiatsmt	pfssvslgagadap	tlsvd	464
RESULT 9					
AAAY23741					
ID	AAAY23741	standard; Protein; 591 AA.			
XX	AC	AAAY23741;			
DT	08-SEP-1999	(first entry)			
XX	A surface protein of Neisseria meningitidis.				
DE	Surface protein; surface glycoprotein; infection; vaccine;				
XX	immunoreactive peptide.				
KW	Neisseria meningitidis.				
XX	WO9931132-A1.				
XX	24-JUN-1999.				
XX	14-DEC-1998; 98WO-AU01031.				
XX	12-DEC-1997; 97GB-0026398.				
XX	(ISIS-) ISIS INNOVATION LTD.				
PA	(UYQU ) UNIV QUEENSLAND.				
XX	Jennings MP, Moxon ER, Peak IRA;				
PI	WPI; 1999-418754/35.				
XX	N-PSDB; AAX85793.				
XX	Neisseria meningitidis surface proteins useful for treating N.				
PT	meningitidis infections				
XX	Claim 1; Page 104-106; 132pp; English.				
PS	The present sequence represents a surface protein of Neisseria				
XX	meningitidis which is approximately 62 kDa. The N. meningitidis				
CC	surface glycoproteins, nucleic acids, the primers and optionally				
CC	a thermostable polymerase, or antibodies are useful in a kit for				
CC	the detection or diagnosis of N. meningitidis infection in humans.				
CC	The N. meningitidis surface glycoproteins can also be used to				
CC	prevent or treat N. meningitidis infection in humans, especially				
CC	in the form of vaccines. The proteins and antibodies can also				
CC	be used to identify immunoreactive peptides.				
XX	Sequence 591 AA;				
SQ					
Query Match					
Best Local Similarity		27.1%; Score 161; DB 20; Length 591;			
Matches 161; Conservative 0;		Mismatches 0; Indels 0; Gaps 0;			
QY	306	GEGLVTAKEVIDAVNKAGWRMKT	TTTANGQTGOADKPFETVTS	GTNVTFFASGKTTATVSKD	365
Db	304	geglvtakevidavnkagwrmtt	tangqtgqadkfetvts	gtntvfaskgttatvskd	363
QY	366	DQGNITVMYDVNVGDALNVNQLNSGWNLD	SKAVAGSSGKVISGNVSPSKGMD	ETVNNIN	425
Db	364	dqgnitvmydvnvgdalnvqnsgwnld	skavagssgkvisgnvpsk	gkmdetvnn	423
QY	426	AGNIEITRNGKNIDIATSMTPQFSSVSLG	AGADAPTL	SVD	466



Db 424 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 464

RESULT 10  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNTVTFASGKGTATVSKD 365  
|||||  
Db 304 geglvtakevidavnkagwrmtttangqtgqadkfetvtsgtntvtfasgkgtatvskd 363  
|||||  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIN 425  
|||||  
Db 364 dqgnitvm ydv nvg dalnvnqlnsgwnldskavagssgkvisgnvspsgkmdetv nin 423  
|||||  
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLUSD 466  
|||||  
Db 424 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 464

RESULT 11  
AAY57045  
ID AAY57045 standard; Protein; 591 AA.  
XX

AC AAY57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 90 /note= "Encoded by AAT"  
FT Misc-difference 92 /note= "Encoded by GAT"  
FT Misc-difference 98 /note= "Encoded by AAC"  
FT Misc-difference 108 /note= "Encoded by AATC"  
FT Misc-difference 123 /note= "Encoded by ACA"  
FT Misc-difference 269 /note= "Encoded by AAA"  
FT Misc-difference 389 /note= "Encoded by CGT"  
XX  
PN WO9958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PE 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39865.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing an immune  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 21; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-149;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GEGLVTAKEVIDAVNKAGWRMKTTHANGQTQADKFETVTSNTVTFASGKGTTATVSKD 365  
 |||||  
 Db 304 geglvtakevidavnkagwrmttttangqtgqadkfetvtsntvtfasgkgttatvskd 363  
 |||||

QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDFTVNIN 425  
 |||||  
 Db 364 dqgnitvmydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpskkgkmdetvnin 423  
 |||||

QY 426 AGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVD 466  
 |||||  
 Db 424 agnnieitrngknidiatsmtpqfssvslgagadapltlsvd 464  
 |||||

RESULT 12  
 AAU06171  
 ID AAU06171 standard; Protein; 591 AA.  
 XX  
 AC AAU06171;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.  
 DE  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW  
 XX Neisseria meningitidis strain PMC21.  
 OS  
 XX

Key Location/Qualifiers  
 FT Peptide 1..51  
 FT /label= Signal\_peptide  
 FT Region 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..108  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 52..591  
 FT /label= Mature\_Nhha  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 FT 109..120  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 121..124  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 125..188  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 189..210  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 211..229  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 230..236  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 237..591  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 XX WO200155182-A1.  
 PN  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-AU000069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYQU ) UNIV QUEENSLAND.  
 PA

XX Peak IRA, Jennings MP;  
 PI  
 XX WPI; 2001-488774/53.  
 DR  
 DR N-PSDB; AAS09161.  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 9; Fig 1; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 SQ Sequence 591 AA;

Query Match 27.1%; Score 161; DB 22; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DT 24-OCT-2001 (first entry)  
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 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW  
 XX Neisseria meningitidis strain EG329.  
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Key Location/Qualifiers  
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 PD 02-AUG-2001.  
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 XX 25-JAN-2001; 2001WO-AU000069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYQU ) UNIV QUEENSLAND.  
 PA

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PN      WO200155182-A1.
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PD      02-AUG-2001.
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PF      25-JAN-2001; 2001WO-AU00069.
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PR      25-JAN-2000; 2000US-0177917.
XX
PA      (UYQU ) UNIV QUEENSLAND.
XX
PI      Peak IRA,  Jennings MP;
XX
WPI; 2001-488774/53.
DR      N-PSDB; AAS09165.
XX
New Nhha surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis -
XX
PS      Claim 9; Fig 1; 9lpp; English.
XX
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen. Nhha
CC      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Nhha
CC      from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX
SQ      Sequence 591 AA;

Query Match      27.1%; Score 161; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT      08-SEP-1999 (first entry)
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DE      A surface protein of Neisseria meningitidis.
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KW      Surface protein; surface glycoprotein; infection; vaccine;
KW      immunoreactive peptide.
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OS      Neisseria meningitidis.
XX
PN      WO9931132-A1.
XX
PD      24-JUN-1999.
XX
PF      14-DEC-1998; 98WO-AU01031.
XX
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISIS-) ISIS INNOVATION LTD.
PA      (UYQU ) UNIV QUEENSLAND.
XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX
WPI; 1999-418754/35.
DR      N-PSDB; AAX85788.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX
PS      Claim 1; Page 86-87; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX
SQ      Sequence 592 AA;

Query Match      27.1%; Score 161; DB 20; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.5e-149;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT      24-OCT-2001 (first entry)
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:36:54 ; Search time 25.54 Seconds  
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568.082 Million cell updates/sec

Title: US-09-700-293-2

Perfect score: 594

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Post-processing: Listing first 1000 summaries

Database : Issued Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	594	100.0	594	4	US-09-669-974-9	Sequence 9, Appli
3	161	27.1	591	4	US-09-377-155-11	Sequence 11, Appl
4	161	27.1	591	4	US-09-377-155-21	Sequence 21, Appl
5	161	27.1	591	4	US-09-669-974-11	Sequence 11, Appl
6	161	27.1	591	4	US-09-669-974-21	Sequence 21, Appl
7	161	27.1	592	4	US-09-377-155-2	Sequence 2, Appli
8	161	27.1	592	4	US-09-669-974-2	Sequence 2, Appli
9	138	23.2	589	4	US-09-377-155-19	Sequence 19, Appl
10	138	23.2	589	4	US-09-669-974-19	Sequence 19, Appl
11	138	23.2	592	4	US-09-377-155-17	Sequence 17, Appl
12	138	23.2	592	4	US-09-669-974-17	Sequence 17, Appl
13	138	23.2	598	4	US-09-377-155-5	Sequence 5, Appli
14	138	23.2	598	4	US-09-377-155-13	Sequence 13, Appl
15	138	23.2	598	4	US-09-669-974-5	Sequence 5, Appli
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17	94	15.8	599	4	US-09-377-155-15	Sequence 15, Appl
18	94	15.8	599	4	US-09-669-974-15	Sequence 15, Appl
19	93	15.7	594	4	US-09-377-155-7	Sequence 7, Appli
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38	20	3.4	607	3	US-08-685-467-6	Sequence 6, Appli
39	20	3.4	607	4	US-08-913-942-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
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US-09-377-155-9

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; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
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; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 100.0%; Score 594; DB 4; Length 594;  
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RESULT 3  
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; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn ver. 2.0  
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; TYPE: PRT  
; LENGTH: 591  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 27.1%; Score 161; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 4  
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; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn ver. 2.0





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RESULT 8  
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; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 27.1%; Score 161; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.3e-144;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 365  
Db 305 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFETVTSGTNVTFAFGKGTATVSKD 364  
QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
Db 365 DQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIN 424  
QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  
Db 425 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 465  
RESULT 9  
US-09-377-155-19  
; Sequence 19, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 589  
; TYPE: PRT

; ORGANISM: Neisseria meningitidis  
US-09-377-155-19  
Query Match 23.2%; Score 138; DB 4; Length 589;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433  
Db 369 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 428  
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSKDANKPVRITNVAPGVKE 493  
Db 429 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSKDANKPVRITNVAPGVKE 488  
QY 494 GDTVNTVAQLKGVAQNLLN 511  
Db 489 GDTVNTVAQLKGVAQNLLN 506  
RESULT 10  
US-09-669-974-19  
; Sequence 19, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 589  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-19

Query Match 23.2%; Score 138; DB 4; Length 589;  
Best Local Similarity 100.0%; Pred. No. 2e-122;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433  
Db 369 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 428  
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSKDANKPVRITNVAPGVKE 493  
Db 429 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSKDANKPVRITNVAPGVKE 488  
QY 494 GDTVNTVAQLKGVAQNLLN 511  
Db 489 GDTVNTVAQLKGVAQNLLN 506  
RESULT 11  
US-09-377-155-17  
; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

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Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
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Db 372 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431
|
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
|
Db 432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 491
|

QY 494 GDTVNTVAQLKGVAQNLLN 511
|
Db 492 GDTVNTVAQLKGVAQNLLN 509
|

RESULT 12
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match 23.2%; Score 138; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
|
Db 372 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 431
|
QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
|
Db 432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 491
|

QY 494 GDTVNTVAQLKGVAQNLLN 511
|
Db 492 GDTVNTVAQLKGVAQNLLN 509
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RESULT 13
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 23.2%; Score 138; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 433
|
Db 378 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNNIEIT 437
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QY 434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 493
|
Db 438 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKE 497
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QY 494 GDTVNTVAQLKGVAQNLLN 511
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Db 498 GDTVNTVAQLKGVAQNLLN 515
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RESULT 14
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 23.2%; Score 138; DB 4; Length 598;





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Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:38:14 ; Search time 33.9 Seconds  
(without alignments)  
1683.689 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	27.1	591	2 G81133	adhesin NMB0992 [i
2	127	21.4	592	2 A81888	probable surface.f

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: G81133  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755  
A;Accession: G81133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-591 <TET>  
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0992

Query Match 27.1%; Score 161; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 8.7e-156;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFEETVTSGTNVTTFASGKGTTATVSKD 365  
|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFEETVTSGTNVTTFASGKGTTATVSKD 363  
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QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
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Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423  
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QY 426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 466  
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Db 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDV 464  
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RESULT 2  
A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C;Accession: A81888  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491  
A;Reference number: A81775; MUID:20222556  
A;Accession: A81888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-592 <PAR>  
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A;Experimental source: serogroup A, strain 22491  
C;Genetics:  
A;Gene: NMA1200

Query Match 21.4%; Score 127; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 5e-121;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFEETVTSGTNVTTFASGKGTTATVSKD 363  
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QY 366 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425  
|||||  
Db 364 DQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423  
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QY 426 AGNNIEI 432  
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Db 424 AGNNIEI 430

Search completed: September 5, 2002, 10:41:54  
Job time: 220 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:41:19 ; Search time 19.15 Seconds  
(without alignments)  
1201.014 Million cell updates/sec

Title: US-09-700-293-2  
Perfect score: 594  
Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: September 5, 2002, 10:48:19  
Job time: 420 sec

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Db 481 PV|RT|NVAPGVKEG|DVT|NVAQLKGVAQN|LN|NHN|D|NVDGNARAGIAQA|A|ATAGLVQAYLPG 540  
QY 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594  
RESULT 2  
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AC Q9JPI3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND BZ232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226376; AAF42525.1; -.  
DR EMBL; AF226369; AAF42518.1; -.  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 37.2%; Score 221; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 4e-204;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 374 YDVNVGDALNVNQLNSGWNLD|SKAVAGSSGKVISGNVSPSKGKMD|ETV|NINAGNNIE|IT 433  
Db 374 YDVNVGDALNVNQLNSGWNLD|SKAVAGSSGKVISGNVSPSKGKMD|ETV|NINAGNNIE|IT 433  
QY 434 R|NGKNIDIAT|SMT|PQFSSVSLGAGADAPT|LSVDDEGALNVGSKDANK|PVRIT|NVAPGVKE 493  
Db 434 R|NGKNIDIAT|SMT|PQFSSVSLGAGADAPT|LSVDDEGALNVGSKDANK|PVRIT|NVAPGVKE 493  
QY 494 G|DVT|NVAQLKGVAQN|LN|NHN|D|NVDGNARAGIAQA|A|ATAGLVQAYLPGKSMMAIGGGTYRG 553  
Db 494 G|DVT|NVAQLKGVAQN|LN|NHN|D|NVDGNARAGIAQA|A|ATAGLVQAYLPGKSMMAIGGGTYRG 553  
QY 554 EAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594  
Db 554 EAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594  
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Q9JPS2  
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AC Q9JPS2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226379; AAF42528.1; -.  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;  
Query Match 37.2%; Score 221; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 4e-204;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 374 YDVNVGDALNVNQLNSGWNLD|SKAVAGSSGKVISGNVSPSKGKMD|ETV|NINAGNNIE|IT 433  
Db 374 YDVNVGDALNVNQLNSGWNLD|SKAVAGSSGKVISGNVSPSKGKMD|ETV|NINAGNNIE|IT 433  
Qy 434 R|NGKNIDIAT|SMT|PQFSSVSLGAGADAPT|LSVDDEGALNVGSKDANK|PVRIT|NVAPGVKE 493  
Db 434 R|NGKNIDIAT|SMT|PQFSSVSLGAGADAPT|LSVDDEGALNVGSKDANK|PVRIT|NVAPGVKE 493  
Qy 494 G|DVT|NVAQLKGVAQN|LN|NHN|D|NVDGNARAGIAQA|A|ATAGLVQAYLPGKSMMAIGGGTYRG 553  
Db 494 G|DVT|NVAQLKGVAQN|LN|NHN|D|NVDGNARAGIAQA|A|ATAGLVQAYLPGKSMMAIGGGTYRG 553  
Qy 554 EAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594  
Db 554 EAGYAIGYSSISDGGNWI|KGTASGNSRGHFGASASVGYQW 594

RESULT 4  
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ID Q9JPH0 PRELIMINARY; PRT; 595 AA.  
AC Q9JPH0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=528, AND 1000;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226360; AAF42509.1; -.  
DR EMBL; AF226356; AAF42505.1; -.  
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;

Query Match		37.2%;	Score 221;	DB 2;	Length 595;
Best Local Similarity		100.0%;	Pred. No. 4e-204;		
Matches 221;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	374	YDVNVGDALNVNQLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVNAGN	IEIT 433
Db	375	YDVNVGDALNVNQLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVNAGN	IEIT 434
QY	434	RNGKNIDIATSMTPQFSSVSLG	AGADAPTL	SVDD	DEGALNVGSKDANKPVRITNVAPGVKE 493
Db	435	RNGKNIDIATSMTPQFSSVSLG	AGADAPTL	SVDD	DEGALNVGSKDANKPVRITNVAPGVKE 494
QY	494	GDVTNVAQLKGVAQNLNHNHID	NVDGNARAGTAAQAIATAGLVQ	AYLP	PGKSMMAIGGTYRG 553
Db	495	GDVTNVAQLKGVAQNLNHNHID	NVDGNARAGTAAQAIATAGLVQ	AYLP	PGKSMMAIGGTYRG 554
QY	554	EAGYAIGYSSISDGGNWI	IKGTASNSR	GHFGASASVGYQW 594	
Db	555	EAGYAIGYSSISDGGNWI	IKGTASNSR	GHFGASASVGYQW 595	
RESULT 5					
Q9JPS9					
ID	Q9JPS9	PRELIMINARY;		PRT;	592 AA.
AC	Q9JPS9;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=860800;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	"Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by Whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
DR	EMBL; AF226361; AAF42510.1; -.				
SQ	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;				
Query Match		27.3%;	Score 162;	DB 2;	Length 592;
Best Local Similarity		100.0%;	Pred. No. 3e-147;		
Matches 162;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	306	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGQT	GQADKFETV	TSGTNVTFASGKGTATVSKD 365
Db	304	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGQT	GQADKFETV	TSGTNVTFASGKGTATVSKD 363
QY	366	DQGNITVMYDVNVGDALNVN	QLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVN 425
Db	364	DQGNITVMYDVNVGDALNVN	QLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVN 423
QY	426	AGNNIEITRNGKNIDIATSM	TPQFSSVSLG	AGADAPTL	SVDD 467
Db	424	AGNNIEITRNGKNIDIATSM	TPQFSSVSLG	AGADAPTL	SVDD 465
RESULT 6					
Q9JPR7					
ID	Q9JPR7	PRELIMINARY;		PRT;	598 AA.
AC	Q9JPR7;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				

Query Match		27.3%;	Score 162;	DB 2;	Length 598;
Best Local Similarity		100.0%;	Pred. No. 3e-147;		
Matches 162;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	310	GEGLVTAKEVIDAVNKAGWRM	KTNTTANGQT	GQADKFETV	TSGTNVTFASGKGTATVSKD 369
QY	366	DQGNITVMYDVNVGDALNVN	QLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVN 425
Db	370	DQGNITVMYDVNVGDALNVN	QLNSGWNLD	SKAVAGSGKVISGNVSPSKGKMD	ETVNVN 429
QY	426	AGNNIEITRNGKNIDIATSM	TPQFSSVSLG	AGADAPTL	SVDD 467
Db	430	AGNNIEITRNGKNIDIATSM	TPQFSSVSLG	AGADAPTL	SVDD 471
RESULT 7					
Q9JPS8					
ID	Q9JPS8	PRELIMINARY;		PRT;	599 AA.
AC	Q9JPS8;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992.				
GN	GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A22;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	"Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by Whole-Genome Sequencing."				
RL	Science 287:1816-1820(2000).				
DR	EMBL; AF226364; AAF42513.1; -.				
SQ	SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;				
Query Match		27.3%;	Score 162;	DB 2;	Length 599;



Best Local Similarity 100.0%; Pred. No. 3e-147;		Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	311	GEGLVTAKEVIDAVNKAGWRMKT	TTANGQTGQADKPE
QY	366	DQGNITVMYDVNVGDALNVNQL	NSQNSGNWLD
Db	371	DQGNITVMYDVNVGDALNVNQL	NSQNSGNWLD
QY	426	AGNNIEITRNGKNIDIATSM	TPQFSSVSLGAGADAPT
Db	431	AGNNIEITRNGKNIDIATSM	TPQFSSVSLGAGADAPT
<p>RESULT 8</p> <p>Q9JPS7 Q9JPS7 PRELIMINARY; PRT; 591 AA.</p> <p>AC Q9JPS7</p> <p>DT 01-OCT-2000 (TReMBLrel. 15, Created)</p> <p>DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)</p> <p>DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)</p> <p>DE OUTER MEMBRANE PROTEIN GNA992.</p> <p>GN GNA992.</p> <p>OS Neisseria meningitidis.</p> <p>OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.</p> <p>OX NCBI_TaxID=487;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RC STRAIN=B2147;</p> <p>RX MEDLINE=20175756; PubMed=10710308;</p> <p>RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,</p> <p>RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,</p> <p>RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,</p> <p>RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zhu P.,</p> <p>RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,</p> <p>RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,</p> <p>RA Moxon E.R., Grandi G., Rappuoli R.;</p> <p>RT "Identification of Vaccine Candidates Against Serogroup B</p> <p>RL Meningococcus by Whole-Genome Sequencing.";</p> <p>RL Science 287:1816-1820(2000).</p> <p>DR EMBL; AF226366; AAF42515.1; -.</p> <p>SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;</p>			

OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
OX	NCBI_TaxID=487;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=EG329;
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT	"Identification and characterization of a gene encoding a novel outer
RL	membrane protein of Neisseria meningitidis.";
DR	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
SQ	EMBL; AF157606; AAK68867.1; -. SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;
	Query Match 27.1%; Score 161; DB 2; Length 591; Best Local Similarity 100.0%; Pred. No. 2.7e-146; Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	306 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFETVTSGTNTVFASGKGTTATVSKD 365 
DB	304 GEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFETVTSGTNTVFASGKGTTATVSKD 363 
QY	366 DQGNTVTMYDVNVGDALNVNLQNLSGNWLDKAVAGSSGKVISGNVSPSGKMDET VNIN 425 
DB	364 DQGNTVTMYDVNVGDALNVNLQNLSGNWLDKAVAGSSGKVISGNVSPSGKMDET VNIN 423 
QY	426 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466 
DB	424 AGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464 
RESULT	10
Q9JR18	
ID	Q9JR18 PRELIMINARY; PRT; 591 AA.
AC	Q9JR18;
DT	01-OCT-2000 (TReMBLrel. 15, Created)
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).
DE	GNA992 OR NMB0992 OR NHHA.
GN	GNA992 OR NMB0992 OR NHHA.
OS	Neisseria meningitidis, and
OS	Neisseria meningitidis (serogroup B).
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX	NCBI_TaxID=487, 491;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;
RX	MEDLINE=20175756; PubMed=10710308;
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zhuo P.,
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA	Moxon E.R., Grandi G., Rappuoli R.;
RT	"Identification of Vaccine Candidates Against Serogroup B
RT	Meningococcus by Whole-Genome Sequencing."
RL	Science 287:1816-1820(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MC58 / SEROGROUP B;
RX	MEDLINE=20175755; PubMed=10710307;
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA	Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA	Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA	Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain
RL	MC58.";
RT	Science 287:1809-1815(2000).







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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:14 ; Search time 58.56 Seconds  
(without alignments)  
1120.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2999	99.9	591	AA1980	Amino acid sequenc
2	2999	99.9	591	AA1981	A surface protein
3	2999	99.9	591	AA1982	N. meningitidis PM
4	2981	99.3	591	AA1983	BASB029 amino acid
5	2980	99.2	591	AA1984	A surface protein
6	2980	99.2	591	AA1985	N. meningitidis EG
7	2967.5	98.8	592	AA1986	A surface protein
8	2762.5	92.0	594	AA1987	A surface protein
9	2762.5	92.0	594	AA1988	BASB029 amino acid
10	2762.5	92.0	594	AA1989	N. meningitidis EG
11	2736.5	91.1	594	AA1990	A surface protein

12	2736.5	91.1	594	AA1991	N. meningitidis B2
13	2721.5	90.6	598	AA1992	A surface protein
14	2721.5	90.6	598	AA1993	N. meningitidis H1
15	2712.5	90.3	598	AA1994	A surface protein
16	2712.5	90.3	598	AA1995	N. meningitidis B2
17	2689	89.5	599	AA1996	A surface protein
18	2689	89.5	599	AA1997	N. meningitidis H3
19	2577.5	85.8	592	AA1998	A surface protein
20	2577.5	85.8	592	AA1999	N. meningitidis H4
21	2546.5	84.8	512	AA2000	N. meningitidis PM
22	2475	82.4	589	AA2001	A surface protein
23	2475	82.4	589	AA2002	N. meningitidis P2
24	2468.5	82.2	592	AA2003	N. meningitidis Z2
25	2455.5	81.8	502	AA2004	N. meningitidis PM
26	2439.5	81.2	592	AA2005	Amino acid sequenc
27	2411	80.3	513	AA2006	N. meningitidis H4
28	2231.5	74.3	604	AA2007	N. meningitidis su
29	2104	70.1	433	AA2008	N. meningitidis PM
30	1957	65.2	407	AA2009	N. meningitidis PM
31	1245	41.5	2411	AA2010	Haemophilus influe
32	1243	41.4	2353	AA2011	Haemophilus adhesi
33	1228	40.9	245	AA2012	Amino acid sequenc
34	1070.5	35.6	1094	AA2013	Haemophilus influe
35	1057.5	35.2	1098	AA2014	Haemophilus adhesi
36	995	33.1	679	AA2015	Haemophilus adhesi
37	995	33.1	679	AA2016	Haemophilus influe
38	752.5	25.1	1004	AA2017	Haemophilus influe
39	741.5	24.7	1002	AA2018	Haemophilus influe
40	696.5	23.2	1104	AA2019	Haemophilus influe
41	696.5	23.2	1104	AA2020	Haemophilus influe
42	600	20.0	116	AA2021	Neisserial conserv
43	388	12.9	2314	AA2022	M. catarrhalis les
44	386.5	12.9	1778	AA2023	Escherichia coli p
45	382	12.7	2123	AA2024	Moraxella catarrha

ALIGNMENTS

RESULT 1  
AA1980  
ID AA1980 standard; Protein; 591 AA.  
XX  
AC AA1980;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9336544-A2.  
XX  
PD 22-JUL-1999.  
XX  
PF 14-JAN-1999; 99WO-IB00103.  
XX  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Grandi G, Massignani V, Pizsa M, Rappuoli R, Scarlato V;  
XX  
DR WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria

PT meningitidis infections  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
CC The invention provides proteins (AAY27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX  
SQ Sequence 591 AA;

Query Match 99.9%; Score 2999; DB 20; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.9e-171;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 mnkiyriiwnsalnawvvvseltrnhtkrasatvktavlatllfatvgasanneeqeedl 60  
  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQ 120  
Db 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekgvltareitlkagdnlkikq 120  
  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 ngtnftyslkkdltdltsvgteklsfngknvntsdtkglnfaketagtngdttvhl 180  
  
QY 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 240  
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QY 241 VRTYDTVEFLSADTKTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDKGENGSS 300  
Db 241 vrt ydtveflsadtktttvnveskdngkktevkigaktsvikekdglvtgkdkgen 300  
  
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Db 301 tdegeglvtakevidavnkagwrmktttangqtgoadkfetvtsgtntvtfasgkgtatv 360  
  
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Db 361 skddqgnitvmydvnvgdalnv nqlqns gwnlds kavgssgkv isgnvsp skgmdetv 420  
  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVDGDALNVGSKKDNKPVR 480  
Db 421 ninagnnieitrngknidiatsmtpqfssvslgagadap tlvsgd alnvgs kkdnpvr 480  
  
QY 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATATAGLVQAYLP GKSM 540  
Db 481 itnvapgvkegdvtnvaqlkgvaqnl nrridnvgnaragi aqaatata glvqaylp gksm 540  
  
QY 541 MAIGGTYRGEAGYAGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 591  
Db 541 maiggtyrgeagayagys sisdgg nwiikg t asgnsrghfgasasvgyqw 591

RESULT 2  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
DT 08-SEP-1999 (first entry).  
XX  
DE A surface protein of *Neisseria meningitidis*.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX

OS *Neisseria meningitidis*.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N.* meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;

Query Match 99.9%; Score 2999; DB 20; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.9e-171;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 mnkiyriiwnsalnawvvvseltrnhtkrasatvktavlatllfatvgasanneeqeedl 60  
  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAAREITLKAGDNLKIKQ 120  
Db 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekgvltareitlkagdnlkikq 120  
  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 ngtnftyslkkdltdltsvgteklsfngknvntsdtkglnfaketagtngdttvhl 180  
  
QY 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 240  
Db 181 gigstltdllntgattnvtndnvtddkkraasvkdvl nagwnkvgkpgttasdnvdf 240  
  
QY 241 VRTYDTVEFLSADTKTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDKGENGSS 300  
Db 241 vrt ydtveflsadtktttvnveskdngkktevkigaktsvikekdglvtgkdkgen 300  
  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKT TTANGQTGOADKFETVTSGTNNVTFASGKGTATV 360  
Db 301 tdegeglvtakevidavnkagwrmktttangqtgoadkfetvtsgtntvtfasgkgtatv 360  
  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETV 420  
Db 361 skddqgnitvmydvnvgdalnv nqlqns gwnlds kavgssgkv isgnvsp skgmdetv 420  
  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP TLSVDGDALNVGSKKDNKPVR 480  
Db 421 ninagnnieitrngknidiatsmtpqfssvslgagadap tlvsgd alnvgs kkdnpvr 480  
  
QY 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATATAGLVQAYLP GKSM 540





XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Nisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 90 /note= "Encoded by AAT"  
FT Misc-difference 92 /note= "Encoded by GAT"  
FT Misc-difference 98 /note= "Encoded by AAC"  
FT Misc-difference 108 /note= "Encoded by AATC"  
FT Misc-difference 123 /note= "Encoded by ACA"  
FT Misc-difference 269 /note= "Encoded by AAA"  
FT Misc-difference 389 /note= "Encoded by CGT"  
XX  
PN WO9958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39865.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing an immune  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 591 AA;

Query Match 99.3%; Score 2991; DB 21; Length 591;  
Best Local Similarity 99.2%; Pred. No. 2.3e-170;  
Matches 586; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNSSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 mnkiyriiwnsalnawavseltrnhtkrasatvktavlatllfatvqasanneegeeel 60  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
Db 61 yldpvqrtvavliivnsdkegtgekekeveedsnwavyfdekgtltareitlkagdnlkikq 120  
QY 121 NGTNFTYSLKKDLTDLTSVGTPEKLSFSGANGKNVNITSDPTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 ngsnftyslkkdltdltsvgteklsfsangknvnitsdptkglnfaketagngdttvhl 180  
QY 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 240  
Db 181 gigstltdllntgattnvtndnvtddkkraasvkdvlnagwnikgvkpgttasdnvdf 240  
QY 241 VRTYDTVEFLSADTKTTTNNVESKDNGKTEVKIGAKTSVKEKDGKLVTKDKGEGSS 300  
Db 241 vrttydtveflsadtktttnnveskdngkrtevkigaktsvikekdgklvtgkdkgegss 300  
QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTITTANGQTGQADKFETVTSGTNVTFASGKGTATV 360  
Db 301 tdegeglvtakevidavnkagwrmktttanggtgqadkftvtsgtntvfaskgttatv 360  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGMDETV 420  
Db 361 skddqgnitvmylvdvnvgdalinvnqlnsgwnlds kavagssgkv isgnvpsk gmdetv 420  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVR 480  
Db 421 ninagnnieitrngknidiatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpv 480  
QY 481 ITNVAPGVKEGDTVNTVAQLKGVQNLNRRIDNVGDNARAGIAQAIATAGLVQAYLPGKSM 540  
Db 481 itnvapgvegdvtnvaqlkgvaqlnnridnvdgnaragiaqaiataglvqaylpgksm 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 591  
Db 541 maigggtyrgeagyaigyssisdggnwiilkgtasgnsrghfgasasvgyqw 591

RESULT 5  
AAY23741  
ID AAY23741 standard; Protein; 591 AA.  
XX  
AC AAY23741;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX (UYQU ) UNIV QUEENSLAND.  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85793.  
XX



Best Local Similarity 99.3%; Pred. No. 2.6e-170;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 mneilriiwnsalnawvvseltrnhtkrasatvktavlatllfatqasanneegeecl 60

Qy 61 YLDPVQRTVAVLIVNSDKEGTEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
Db 61 yldpvlrtvavlivnsdkegtekekeveensdwavyfnekgvltareitlkagdnlkikq 120

Qy 121 NGTNFTYSLKKDLTDLTSVGTSEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTFVHLN 180  
Db 121 ngtnftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketagntgdtttvhl 180

Qy 181 GIGSTLFTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 240  
Db 181 gigstlftdllntgattnvtndnvtddkkraasvkdvl nagwnikgvkpgttasdnvdf 240

Qy 241 VRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVGTGKDKGENGSS 300  
Db 241 vrt ydtveflsadtktttv nveskdngkktevki gaktsvikekdgklvtgkdkgen gss 300

Qy 301 TDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGQADKFETVTSGTNVTFASGKGTTATV 360  
Db 301 tdegeglvtakevidavnkagwr mktttangqtgqadkfetvtsgtntvtfasgkgttatv 360

Qy 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETV 420  
Db 361 skddqgnitvm ydvnvgdalnv nqlnsgwnldskavagssgkv isgnvspskgmdetv 420

Qy 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDNKPV 480  
Db 421 ninagnnieitrngknidiat smtpqfssvslgagadap tlvsgdalnv gskdnkpv 480

Qy 481 ITNVAPGVKEGDTVNAQLKGVAQNLRIDNVGDNARAGIAQAIATAGLVQAYLPQKSM 540  
Db 481 itnvapgvkegdvtnvaqlkgvaq nlrnidnv gdnarag iaqaiataglvqaylpqks m 540

Qy 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 maigggtyrgeag yaigyssisd ggnwiikgtas gnsrghfgasasvgyqw 591

RESULT 7  
AAY23737  
ID AAY23737 standard; Protein; 592 AA.  
XX  
AC AAY23737;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.

DR N-PSDB; AAX85788.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX Claim 1; Page 86-87; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 592 AA;

Query Match 98.8%; Score 2967.5; DB 20; Length 592;  
Best Local Similarity 98.8%; Pred. No. 1.4e-169;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEED 59  
Db 1 mnkiyriiwnsalnawvvseltrnhtkrasatvktavlatllfatvqasannerprkdd 60

Qy 60 LYLDPVQRTVAVLIVNSDKEGTEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119  
Db 61 yldpvrqtrtavlivnsdkegtekekeveensdwavyfnekgvltareitlkagdnlkik 120

Qy 120 QNGTNFTYSLKKDLTDLTSVGTSEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHL 179  
Db 121 qngtnftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketagntgdtvhl 180

Qy 180 NGIGSTLTDTLTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTTASDNVD 239  
Db 181 ngigstltdtllntgattnvtndnvtddkkraasvkdvl nagwnikgvkpgttasdnvd 240

Qy 240 FVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVGTGKDKGENGS 299  
Db 241 fvrt ydtveflsadtktttv nveskdngkktevki gaktsvikekdgklvtgkdkgen gs 300

Qy 300 STDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGQADKFETVTSGTNVTFASGKGTTAT 359  
Db 301 stdegeglvtakevidavnkagwr mktttangqtgqadkfetvtsgtntvtfasgkgttat 360

Qy 360 VSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDET 419  
Db 361 vskddqgnitvm ydvnvgdalnv nqlnsgwnldskavagssgkv isgnvspskgkmdet 420

Qy 420 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDNKPV 479  
Db 421 vninagnnieitrngknidiat smtpqfssvslgagadap tlvsgdalnv gskdnkpv 480

Qy 480 RITNVAPGVKEGDTVNAQLKGVAQNLRIDNVGDNARAGIAQAIATAGLVQAYLPGKS 539  
Db 481 ritnvapgvkegdvtnvaqlkgvaq nlrnidnv gdnarag iaqaiataglvqaylpgks 540

Qy 540 MMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 mmaigggtyrgeag yaigyssisd ggnwiikgtas gnsrghfgasasvgyqw 592

RESULT 8  
AAY23740  
ID AAY23740 standard; Protein; 594 AA.  
XX  
AC AAY23740;  
XX  
DT 08-SEP-1999 (first entry)  
XX



DE A surface protein of Neisseria meningitidis.  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections

PS Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

Query Match 92.0%; Score 2762.5; DB 20; Length 594;  
Best Local Similarity 92.5%; Pred. No. 2.6e-157;  
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| : :|||  
1 mnkiyriiwnsalnawavseltrnhtkrasatvatavlatllfatvqasttd---dddl 57

QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLRTAREITLKGADNLKIKQ 120  
Db ||||||| || ||||||| || ||:| ||:||||| ||||||| ||||||| |||||||  
58 ylepvqrtavvlfrsdkegtgeke-vtedsnwgyvfdkkgvltagtitlkgadnlkikq 116

QY 121 -----NGTNFTYSLKKDLTDLTTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGD 174  
Db | :||||| ||||||| ||||||| ||||||| ||||||| ||||||| : :|||  
117 ntntentnassftyslkkdltdltsvgteklsfsansknvnitsdtkglnfakaktaetngd 176

QY 175 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 234  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
177 ttvhlngigstltdtllntgattntvndntddekraasvkdvl nagwnikgvkpgtta 236

QY 235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVGTGDK 294  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
237 sdnvdfvrttydtveflsadtktttnvveskdngkrtevkigaktsvikekdgklvtgdk 296

QY 295 GENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGGADKFETVTSGTNVTFASGK 354  
Db || ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
297 gendsstkdeglvtakevidavnkagwrmtttangtggadkfetvtsgtntvtfasgk 356

QY 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
357 gttatvskddqgnitvmydvnvvgdalnvnqlnsgwnldskavagssgkvisgnvspkg 416

QY 415 KMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLTSDGD-ALNVGSK 473  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| : |||||||  
417 kmdetvniagnnieitrngknidiatsmtptqfssvslgagadaptlsvddegainvsgk 476  
QY 474 KDNKPVRITNVAPGVKEGVTNVAQLKGVAQNLNNRIDNVGNARAGIAQAIAATAGLVQA 533  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
477 dankpvrितnvapgvkegvtvnvaqlkgvaqnlhnhidnvdgnaragiaqaiaataglvqa 536  
QY 534 YLPKGSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKTASGNSRHFSGASASVGYQW 591  
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
537 ylpkgsmmaiggtyrgeagyaigyssisdggnwiiktasgnsrghfgasasvgyqw 594  
RESULT 9  
AAAY57044  
ID AAY57044 standard; Protein; 594 AA.  
XX  
AC AAY57044;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 104 /note= "Encoded by AATC"  
FT  
XX  
PN WO9958683-A2.  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39864.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX









```
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 90.6%; Score 2721.5; DB 20; Length 598;
Best Local Similarity 90.9%; Pred. No. 7.5e-155;
Matches 547; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
Db 1 mnkiyriiwnlsalnawvvsvseltrnhtrkrasatvatavlatllfatvqanatd---dddl 57

QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
Db 58 ylepvqrtavvlfrsrdkegtgekted-snwavyfdekrvfkagaitlkagdnlkikq 116

QY 121 -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAG 170
Db 117 ntntentntndssftyslkkdltdltsveteklsfgangknvnitsdtkglnfaketag 176

QY 171 TNGDTTVHLNGIGSTLTDTLLNTGATTNVNTDNDVTDDEKKRAASVKDVLNAGWNIKGVKP 230
Db 177 tngdptvhlngigstltdtllntgattnvndndvtddekkraasvkdvlnagwnikgvkp 236

QY 231 GTTASDNVDVFRTYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGLVT 290
Db 237 gttasdnvdfvrttydveflsadtktttvnveskdngkktevkigaktsvikekdgklvt 296

QY 291 GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTF 350
Db 297 gkgkdengsstdegeglvtakevidavnkagwrmktttanggtggadkfetvtsgtkvtf 356

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QY 590 QW 591
Db 597 qw 598

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XX
AC AAU06177;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H15 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H15.
XX
FH Key Location/Qualifiers
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FT /label= C1
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FT /note= "Variable region 1"
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FT /note= "Variable region 4"
FT 243..598 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
XX
N-PSDB; AAS09167.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 598 AA;
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Query Match 90.6%; Score 2721.5; DB 22; Length 598;
Best Local Similarity 90.9%; Pred. No. 7.5e-155;
Matches 547; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

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QY 590 QW 591  
||  
Db 597 qw 598

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AC AAY23738;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
DR N-PSDB: AAX85790.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections  
XX  
PS Claim 1; Page 91-93; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
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SQ Sequence 598 AA;

Query Match 90.3%; Score 2712.5; DB 20; Length 598;  
Best Local Similarity 90.5%; Pred. No. 2.6e-154;  
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:46 ; Search time 25.63 Seconds  
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Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2980	99.2	591	US-09-669-974-11	Sequence 11, Appl
5	2967.5	98.8	592	US-09-377-155-2	Sequence 2, Appl
6	2967.5	98.8	592	US-09-669-974-2	Sequence 2, Appl
7	2762.5	92.0	594	US-09-377-155-9	Sequence 9, Appl
8	2762.5	92.0	594	US-09-669-974-9	Sequence 9, Appl
9	2736.5	91.1	594	US-09-377-155-7	Sequence 7, Appl
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11	2721.5	90.6	598	US-09-377-155-13	Sequence 13, Appl
12	2721.5	90.6	598	US-09-669-974-13	Sequence 13, Appl
13	2712.5	90.3	598	US-09-377-155-5	Sequence 5, Appl
14	2712.5	90.3	598	US-09-669-974-5	Sequence 5, Appl
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16	2689	89.5	599	US-09-669-974-15	Sequence 15, Appl
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22	1243	41.4	2353	US-09-377-155-33	Sequence 33, Appl
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24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
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35	1057.5	35.2	1098	4	US-08-913-942-2	Sequence 2, Appl
36	1057.5	35.2	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1057.5	35.2	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1039.5	34.6	658	1	US-08-409-995-5	Sequence 5, Appl
39	1039.5	34.6	658	3	US-08-685-467-5	Sequence 5, Appl
40	1039.5	34.6	658	4	US-08-913-942-5	Sequence 5, Appl
41	995	33.1	679	4	US-08-913-942-15	Sequence 15, Appl
42	995	33.1	679	4	US-09-268-347-26	Sequence 26, Appl
43	752.5	25.1	1004	4	US-09-268-347-30	Sequence 30, Appl
44	741.5	24.7	1002	4	US-09-268-347-24	Sequence 24, Appl
45	696.5	23.2	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB-9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

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Best Local Similarity	99.8%	Pred. No.	6.7e-225							
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Db	121	NGTNFTYSLKKDLTSLTSVGTSEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN	180							
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QY	301	TDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSCTNVTFASGKGTTATV	360							

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Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKPVR 480  
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Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYOW 591

RESULT 2

US-09-669-974-21

; Sequence 21, Application US/0966974

; Patent No. 6,495,345

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-21

Query Match 99.9%; Score 2999; DB 4; Length 591;  
Best Local Similarity 99.8%; Pred. No. 6.7e-225;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKPVR 480  
Db 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKPVR 480  
QY 481 ITNVAPGVKEGDVTNVQAQLKGVAQNLRNIDNVNVDGNARAGIAQAATAGLVQAYLPGKSM 540  
Db 481 ITNVAPGVKEGDVTNVQAQLKGVAQNLRNIDNVNVDGNARAGIAQAATAGLVQAYLPGKSM 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYOW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYOW 591

RESULT 3

US-09-377-155-11

; Sequence 11, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-11

Query Match 99.2%; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.3%; Pred. No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLTLFATVQASANNEEQEEDL 60  
Db 1 MNEILRIIWNALNAWVSELTRNHTKRASATVKTAVLATLTLFATVQASANNEEQEEDL 60  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120  
Db 61 YLDPVLRVAVLIIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
Db 181 GIGSTLTDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKKGENGSS 300  
Db 241 VRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKKGENGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSNTVTFASGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSNTVTFASGKGTATV 360  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDTV 420



Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVR 480  
Db 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVR 480  
QY 481 ITNVAPGVKEGDTVNVQALKGVAQNLRNDRIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540  
Db 481 ITNVAPGVKEGDTVNVQALKGVAQNLRNDRIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 4  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6,653,173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 99.2%; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.3%; Pred. No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 MNEILRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120  
Db 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDITVHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDITVHLN 180  
QY 181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDF 240  
Db 181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGDKGGENGSS 300  
Db 241 VRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGDKGGENGSS 300  
QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVTSCTNVTFSAGKGTATV 360  
Db 301 TDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVTSCTNVTFSAGKGTATV 360  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDTV 420

Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVR 480  
Db 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVR 480  
QY 481 ITNVAPGVKEGDTVNVQALKGVAQNLRNDRIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540  
Db 481 ITNVAPGVKEGDTVNVQALKGVAQNLRNDRIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540  
QY 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 5  
US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6,197,312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 98.8%; Score 2967.5; DB 4; Length 592;  
Best Local Similarity 98.8%; Pred. No. 1.9e-222;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEED 59  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEPRKKD 60  
QY 60 YLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119  
Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120  
QY 120 QNGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDITVHL 179  
Db 121 QNGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDITVHL 180  
QY 180 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVD 239  
Db 181 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVD 240  
QY 240 FVRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGDKGGENGS 299  
Db 241 FVRTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGDKGGENGS 300  
QY 300 STDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVTSCTNVTFSAGKGTAT 359  
Db 301 STDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFFETVTSCTNVTFSAGKGTAT 360  
QY 360 VSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDET 419  
Db 361 VSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDET 420  
QY 420 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPV 479

Db 421 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
QY 480 RITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVVDGNARAGIAQAIAATAGLVQAYLPGKS 539  
Db 481 RITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVVDGNARAGIAQAIAATAGLVQAYLPGKS 540  
QY 540 MMAIGGGTYRGEAGYAIGYSSISDGGNNWIKGTASGNSRGHFGASASVGYQW 591  
Db 541 MMAIGGGTYRGEAGYAIGYSSISDGGNNWIKGTASGNSRGHFGASASVGYQW 592

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 98.8%; Score 2967.5; DB 4; Length 592;  
Best Local Similarity 98.8%; Pred. No. 1.9e-222;  
Matches 585; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWNALSALNAWVAVSELTRNHTKRASATVKTAVLATLLLFATVOASANNEE-QEED 59  
Db 1 MNKIYRIIWNALSALNAWVAVSELTRNHTKRASATVKTAVLATLLLFATVOASANNERPRKDD 60  
QY 60 LYLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119  
Db 61 LYLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120  
QY 120 QNGTNFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 179  
Db 121 QNGTNFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 180  
QY 180 NGIGSTLDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNVD 239  
Db 181 NGIGSTLDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTASDNVD 240  
QY 240 FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGDKGENGS 299  
Db 241 FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGDKGENGS 300  
QY 300 STDEGEGLVTAKEVIDAVNKAGWRMKTATTANGOTQOQADKFETVTSGTNVTFASGKGTAT 359  
Db 301 STDEGEGLVTAKEVIDAVNKAGWRMKTATTANGOTQOQADKFETVTSGTNVTFASGKGTAT 360  
QY 360 VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDDET 419  
Db 361 VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDDET 420  
QY 420 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 479

Db 421 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
QY 480 RITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVVDGNARAGIAQAIAATAGLVQAYLPGKS 539  
Db 481 RITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVVDGNARAGIAQAIAATAGLVQAYLPGKS 540  
QY 540 MMAIGGGTYRGEAGYAIGYSSISDGGNNWIKGTASGNSRGHFGASASVGYQW 591  
Db 541 MMAIGGGTYRGEAGYAIGYSSISDGGNNWIKGTASGNSRGHFGASASVGYQW 592

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 92.0%; Score 2762.5; DB 4; Length 594;  
Best Local Similarity 92.5%; Pred. No. 1.6e-206;  
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWNALSALNAWVAVSELTRNHTKRASATVKTAVLATLLLFATVOASANNEEQEEDL 60  
Db 1 MNKIYRIIWNALSALNAWVAVSELTRNHTKRASATVKTAVLATLLLFATVQASTTD---DDDL 57  
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120  
Db 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAAGTITLKAGDNLKIK 116  
QY 121 -----NGTNFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKETAGTNGD 174  
Db 117 NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFANGNKVNITSDTKGLNFAKKTAEETNGD 176  
QY 175 TTVHLNGIGSTLDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 234  
Db 177 TTVHLNGIGSTLDTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGWNIKGVPKPGTTA 236  
QY 235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGKDK 294  
Db 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKRTEVKIGAKTSVIKEKDGLVTGKDK 296  
QY 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTATTANGOTQOQADKFETVTSGTNVTFASGK 354  
Db 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTATTANGOTQOQADKFETVTSGTNVTFASGK 356  
QY 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
Db 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
QY 415 KMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSK 473  
Db 417 KMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSK 476  
QY 474 KDNKPVRTNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVVDGNARAGIAQAIAATAGLVQA 533

Db	477	DANKPVRITN	APGVKEGDVT	NAQLKGVAQN	LNHNHIDNV	DGNRAGIAQ	AIATAGLVQA	536
Qy	534	YLPGKSMA	IGGGTYRGE	AGYAICYSS	ISDGGNWI	IKGTASGNS	RGHFGASASV	QYW 591
Db	537	YLPGKSMA	IGGGTYRGE	AGYAICYSS	ISDGGNWI	IKGTASGNS	RGHFGASASV	QYW 594

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RESULT      8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

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	Query Match	92.0%;	Score 2762.5;	DB 4;	Length 594;
	Best Local Similarity	92.5%;	Pred. No. 1.6e-206;		
	Matches 553;	Conservative 14;	Mismatches 20;	Indels 11;	Gaps 4;
QY	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL	60		
Db	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVATAVLATLLFATVQASTTD--DDDL	57		
QY	61	YLDPVQRTAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ	120		
Db	58	YLEPVQRTAVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ	116		
QY	121	-----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGD	174		
Db	117	NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGD	176		
QY	175	TTVHLNGIGSTLTDTLNLTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKIGVKPGTTA	234		
Db	177	TTVHLNGIGSTLTDTLNLTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKIGVKPGTTA	236		
QY	235	SDNVDFVRTYDTEVFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGLVTGKDK	294		
Db	237	SDNVDFVRTYDTEVFLSADTKTTTVNVESKDNKKRTEVKIGAKTSVIKEKDGLVTGKDK	296		
QY	295	GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFFASGK	354		
Db	297	GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFFASGK	356		
QY	355	GTTATVSKDDQGNITVMYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG	414		
Db	357	GTTATVSKDDQGNITVMYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNVSPSKG	416		
QY	415	KMDETVNINAGNNIEITRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALNVGSK	473		
Db	417	KMDETVNINAGNNIEITRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDEGALNVGSK	476		
QY	474	KDNKPVRIITNVAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAGLVQA	533		

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Db      477 DANKPVRITN VAPGVKEGDVTNVNAQLKGV AQNLNNHIDVNDGNARAGTAAQIATAGLVQA 536
QY      534 YLP GKSMMAIGGTYRGEAGYAIGYSSISDGGNWIIKG TASGNSRGHFEGASASVG YQW 591
          |||||
Db      537 YLP GKSMMAIGGTYRGEAGYAIGYSSISDGGNWIIKG TASGNSRGHFEGASASVG YQW 594
          |||||

RESULT          9
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

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Query Match	91.1%;	Score 2736.5;	DB 4;	Length 594;
Best Local Similarity	92.0%;	Pred. No. 1.6e-204;		
Matches 550;	Conservative 11;	Mismatches 26;	Indels 11;	Gaps 4;

QY	1	MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTVATLTLFATVQASANNEEQEEDL	60
DG	1		:
QY	61	YLDPVQRTVAVLIVNSDKBGTGEKEKVEENSDWAVFYFNEKGVLTAAREITLKAGDNLKIKQ	120
DG	58	YLEPVRTAVLSFRSDRGTEGEGTED-SNWAVYFDERKRVLKAGAITLKAGDNLKIKQ	116
QY	121	-----NGTNFTYSLLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGD	174
DG	117	NTNENTNDSSFTYSLLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD	176
QY	175	TTVHLNGIGSTLTDTLLNTGATTNVTDNVTDDEKKRAASVKDVNLNAGWNKGVKPGTTA	234
DG	177	PTVHLNGIGSTLTDTLLNTGATTNVTDNVTDDEKKRAASVKDVNLNAGWNKGVKPGTTA	236
QY	235	SDNVDFVRDYDTVEFLSADTKTTNVNVESKDNGKKTVEKIGAKTSVIKEKDGLVTGDKK	294
DG	237	SDNVDFVRDYDTVEFLSADTKTTNVNVESKDNGKKTVEKIGAKTSVIKEKDGLVTGDKK	296
QY	295	GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGK	354
DG	297	DENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTGOADKFETVTSGTNVTFASGK	356
QY	355	GTTATVSKDDQGNITVMYDVNVGDALNVQLONGSWNLDSKAVAGSSGKVISGNVSPSKG	414
DG	357	GTTATVSKDDQGNITVKYDVNVGDALNVQLONGSWNLDSKAVAGSSGKVISGNVSPSKG	416
QY	415	KMDETVINAGNNIEITRNCKNIDIATSMTPQFESSVSLGACADAPTLSDVDGD-ALNVGSK	473
DG	417	KMDETVINAGNNIEITRNCKNIDIATSMAPQFESSVSLGACADAPTLSDVDEGALNVGSK	476
QY	474	KDNKPVRITNVAPGVKEGDTVNVQAOLKGVAQNLNNRIDNVDCGNARAGIAQAIAATAGLVQA	533
DG	477	DTNKPVRITNVAPGVKEGDTVNVQAOLKGVAQNLNNRIDNVDCGNARAGIAQAIAATAGLVQA	536
QY	534	YLPGKSMAAIGGGTYRGEAGYAIGYSSISDGGNWIICKTAGSNRSGHFHGASASVGYOW	591









Db 537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVG 596  
QY 590 QW 591  
Db 597 QW 598  
  
RESULT 14  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 90.3%; Score 2712.5; DB 4; Length 598;  
Best Local Similarity 90.5%; Pred. No. 1.2e-202;  
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;  
  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 MNKISRIIWNLSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQANATD---DDDL 57  
  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKVEENSQWAVYFNEKGVLTAAREITLKAGDNLKIKQ 120  
Db 58 YLEPVQRTAVVLSFSDKEGTGEKGTED-SNWAYVFDEKRVLKAGAITLKAGDNLKIKQ 116  
  
QY 121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFGSANGNKVNITSDTKGLNFAKETAG 170  
Db 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGNKVNITSDTKGLNFAKETAG 176  
  
QY 171 TNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 230  
Db 177 TNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 236  
  
QY 231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 290  
Db 237 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 296  
  
QY 291 GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVSGTNVTF 350  
Db 297 GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVSGTKVTF 356  
  
QY 351 ASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410  
Db 357 ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 416  
  
QY 411 PSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDGD-ALN 469  
Db 417 PSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALN 476  
  
QY 470 VGSKKDNKPVIRITNVAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAG 529  
|||||

Db 477 VGSKDANKPVRITNVAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAG 536  
QY 530 LVOAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVG 589  
Db 537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVG 596  
QY 590 QW 591  
Db 597 QW 598  
  
RESULT 15  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 89.5%; Score 2689; DB 4; Length 599;  
Best Local Similarity 89.5%; Pred. No. 8.1e-201;  
Matches 539; Conservative 16; Mismatches 33; Indels 14; Gaps 4;  
  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEE- 59  
  
QY 61 YLDPVQRTVAVLIIVNSDKEGTGEKEKVEENSQWAVYFNEKGVLTAAREITLKAGDNLKIKQ 120  
Db 60 -LEPVRSALVLFQFMIDKEGNGENEST-GNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQ 117  
  
QY 121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFGSANGNKVNITSDTKGLNFAKETAG 170  
Db 118 NTNKNTNENTNDSSFTYSLKKDLTDLTSVEIEKLSFGANGNKVNITSDTKGLNFAKETAG 177  
  
QY 171 TNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 230  
Db 178 TNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 237  
  
QY 231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 290  
Db 238 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKRTVEVKIGAKTSVKEKDGKLV 297  
  
QY 291 GKDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVSGTNVTF 350  
Db 298 GKDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFFETVSGTNVTF 357  
  
QY 351 ASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410  
Db 358 ASGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 417  
  
QY 411 PSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVG-DALN 469  
Db 418 PSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKGALN 477  
  
QY 470 VGSKKDNKPVIRITNVAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAG 529

Db 478 V G S K D A N K P V R I T N V A P G V K E G D V T N V A Q L K G V A Q N L N N R I D N V D G N A R A G I A Q A I A T A G 537  
QY 530 L V Q A Y L P G K S M M A I G G G T Y R G E A G Y A I G Y S S I S D G G N W I I K G T A S G N S R G H F G A S A S V G Y 589  
Db 538 L V Q A Y L P G K S M M A I G G G T Y R G E A G Y A I G Y S S I S D G G N W I I K G T A S G N S R G H F G A S A S V G Y 597  
QY 590 QW 591  
Db 598 QW 599

Search completed: September 5, 2002, 10:23:48  
Job time: 285 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2002, 10:24:32 ; Search time 34.15 Seconds  
(without alignments)  
1662.922 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVGQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	99.9	591	2 G81133	adhesin NMB0992 [i
2	2468.5	82.2	592	2 A81888	probable surface f
3	605	20.1	298	2 I64138	adhesin homolog HI
4	393	13.1	2059	2 D82671	surface protein XF
5	378	12.6	1107	2 AC0976	probable autotrans
6	371.5	12.4	1190	2 A82615	surface protein XF
7	363	12.1	1588	2 A86036	probable adhesin Z
8	363	12.1	1588	2 H91188	probable adhesin E
9	331.5	11.0	658	2 AH0110	probable surface p
10	240.5	8.0	1004	2 C82672	surface-exposed ou
11	235.5	7.8	1091	2 G64964	hypothetical prote
12	232.5	7.7	1536	2 A43855	high-molecular-wei
13	221	7.4	1477	2 B43855	high-molecular-wei
14	221	7.4	2020	2 C48399	ABC-type transport
15	219	7.3	1910	2 AF0394	probable adhesin h
16	214	7.1	4919	2 T31105	hypothetical prote
17	213.5	7.1	5291	2 F90696	hypothetical prote
18	212.5	7.1	1286	2 S28634	adhesin AIDA-I pre
19	212	7.1	949	2 D90803	Aida-I adhesin-lik
20	212	7.1	1005	2 H85611	probable adhesin Z
21	212	7.1	1635	2 AI0452	hemolysin [importe
22	211	7.0	1109	2 A56143	surface-array prot
23	210	7.0	1325	2 A64905	ydeK protein - Esc
24	209	7.0	2273	2 T09083	hemagglutinin/hemo
25	208.5	6.9	936	2 I40711	sapB protein - Cam
26	208.5	6.9	1018	2 H83135	probable adhesin p
27	207.5	6.9	1577	2 A35140	hemolysin A precur
28	207.5	6.9	4152	2 T31102	filamentous hemagg
29	207	6.9	5188	2 B85547	probable RTX famil

30	200.5	6.7	1343	2 D85724	hypothetical prote
31	199	6.6	1461	2 E90696	hypothetical prote
32	198.5	6.6	1487	2 AG2560	hypothetical prote
33	197.5	6.6	1343	2 E90893	hypothetical prote
34	197	6.6	585	2 F90961	flagellin [importe
35	197	6.6	585	2 F85809	hypothetical prote
36	195	6.5	1461	2 A85547	hypothetical prote
37	194.5	6.5	1428	2 AC2224	hypothetical prote
38	194.5	6.5	3029	2 S76109	hypothetical prote
39	194	6.5	3705	2 AD0123	probable autotrans
40	193.5	6.4	3013	2 AB0480	probable invasin Y
41	193.5	6.4	4936	2 AH2515	hypothetical prote
42	192	6.4	1430	2 AF0351	probable autotrans
43	191.5	6.4	1335	2 T17508	glycoprotein Vp260
44	191.5	6.4	1608	2 A28182	hemolysin A - Serr
45	191	6.4	2249	2 A41477	190K surface antig

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: G81133  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755  
A;Accession: G81133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-591 <TET>  
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0992

Query Match 99.9%; Score 2999; DB 2; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.3e-140;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWAVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60

Db 1 MNKIYRIIWNLSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60

QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVFNEKGVLTAAREITLKAGDNLKIKQ 120

Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVFNEKGVLTAAREITLKAGDNLKIKQ 120

QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180

Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180

QY 181 GIGSTLTDLLNTGATTNVTDNDVTDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 240

Db 181 GIGSTLTDLLNTGATTNVTDNDVTDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDF 240

QY 241 VRTYDTVFEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVIKEKDGLVTGKDKGENGSS 300

Db 241 VRTYDTVFEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVIKEKDGLVTGKDKGENGSS 300

QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTATV 360

Db 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTFASGKGTTATV 360

QY 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETV 420

Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDTV 420  
QY 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKKDNKPV 480  
Db 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKKDNKPV 480  
QY 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPCKSM 540  
Db 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPCKSM 540  
QY 541 MAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match 82.2%; Score 2468.5; DB 2; Length 592;  
Best Local Similarity 84.4%; Pred. No. 1.7e-114;  
Matches 507; Conservative 30; Mismatches 45; Indels 19; Gaps 8;  
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Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEEEEE- 59  
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVE-ENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119  
Db 60 -LESQRSV-VGSIQASMEGSGELEFISLMTNDSKEFVDPYIV---VTLKAGDNLKIK 113  
QY 120 Q-----NGTNFTYSLKKDLTDLTSVGTCKLSFANGKNVNITSDTKGLNFAKETAGTNG 173  
Db 114 QNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNG 173  
QY 174 DTTVHLNGIGSTLTDTLLNTGATTNVTDNVTDDKRAASVKDVLNAGWNKGVKPGTT 233  
Db 174 DTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKGVKTGST 231  
QY 234 A--SDNVDFVRTYDVFELSDATKTTNVNVEKDKNGKKTEVKIGAKTSVIKEKDKLVTG 291  
Db 232 TGQSENVDFVRTYDVFELSDATKTTNVNVEKDKNGKRTEVKIGAKTSVIKEKDKLVTG 291  
QY 292 KDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGPNVTFA 351  
Db 292 KGKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGPNVTFA 351  
QY 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411  
Db 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411  
QY 412 SKGKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVGDA-ALNV 470  
Db 412 SKGKMDETVNIAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNV 471

QY 471 GSKKDNKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGL 530  
Db 472 GSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGL 531  
QY 531 VQAYLPCKSMMAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 590  
Db 532 VQAYLPCKSMMAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 591  
QY 591 W 591  
Db 592 W 592  
RESULT 3  
I64138  
adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:gl574588; PID:gl574589; TIGR:H11732  
Query Match 20.1%; Score 605; DB 2; Length 298;  
Best Local Similarity 45.9%; Pred. No. 4.4e-23;  
Matches 145; Conservative 42; Mismatches 93; Indels 36; Gaps 8;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNRQEEDL 60  
Db 1 MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQA----- 49  
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK- 119  
Db 50 -INDAGTFVKVQSTEDDIEDSAATK--DDNKNQALKAGD-----TLTLKAGKNLKAKL 99  
QY 120 -QNGTNFTYSLKKDLTDLTSVGTCKLSFSAN-----GNKNVITSDTKGLNFAKETAGT 171  
Db 100 DQGGKSVTFALAKDLDVKTAKVSDTLTIGGNTPAAGGATPKVSTITSTADGLKLAK---GT 156  
QY 172 NGDPTVHLNGIGSTLTDTLLNTGATTNVTDNVTDDKRAASVKDVLNAGWNKGVKPG 231  
Db 157 NGDTAVHLNGLASTLPDVTNTTGASTSVT-FSPSDIEKTRAATIKDVLNAGWNKGA 215  
QY 232 TTASDNVDFVRTYDVFELSDATKTTNVNVEKDKNGKKTEVKIGAKTSVIKEKDKLVTG 291  
Db 216 GGNTENVDLVAGYDNVEFITGDKNTLDVVLTAENGKKTTEVKPTSVIKDNNNGKLLTG 275  
QY 292 KD--KGENGSTDEGE 305  
Db 276 KQLKDANTGTATNATE 291

RESULT 4  
D82671  
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below





Db 862 ENGIGDIVTTGSKYFKTNTDGDADANAQADSAIGSGSIAAAENSVALGTNSVADEANT 921

Qy 468 LNVGSKKDNKPVRTTNVAPGVKEGDTVNTVAQLK----- 500

Db 922 VSVGSSTQQR--RITNVAAGVNNTDVAVNAQLKASEAGSVRYETNADGSVNVSVNLGDLG 979

Qy 501 -----GVAQ-----NLNNRIDNVGDNARAGIAQ 523

Db 980 SGGTRIGNVSAAVNDTDAVNYAQLKRSVEEANTYTDQKMGEMNSKIKGIENKMSGGIAS 1039

Qy 524 AIATAGLVQAYLPCKSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGA 583

Db 1040 AMAMAGLPQAYAPCANMTSIAGTENGESAVAIGVSMVSESGGWYKLGQTSNSQGDYSA 1099

Qy 584 SASVGQYW 591

Db 1100 AIGAGQW 1107

RESULT 6

A82615

surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: A82615

R:anonymouse, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SW>

A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1981

Query Match 12.4%; Score 371.5; DB 2; Length 1190;

Best Local Similarity 23.5%; Pred. No. 8.1e-11;

Matches 167; Conservative 88; Mismatches 243; Indels 213; Gaps 28;

Qy 17 VAVSELTRNHTKRASATVKTAVALTLLFATVOASANNEEQEEDLYLDPVQRT-----VAV 71

Db 557 VTSSGISAGNOKITNVAAGTADTDVAVNFSQLQAVSSTASKGWNLLASGANSSNVVPGESV 616

Qy 72 LIVNSDKEGTEKEKEVEENSDWAVYFNEKGVLTAREIT-----LKAGDNLIKQN 121

Db 617 DLKNSD--GNLLITKTTDSND--VTFNLATALKVDLSLTGTNTAMTTDGVTVGSNVTLGST 672

Qy 122 GTNFTYSLKKDLTDLTSVGTEKLSFSANGKNV-NI---TSDTKGLNFA----- 165

Db 673 GLVIT-----DGPSVTSSG-----ISAGNQKITNVAAGTADTDVAVNFSQLQAVSSTASKG 722

Qy 166 -----KETAG----- 178

Db 723 WNLLASGANSSNVAPGESVDLKNTDGNIVISKESGSDVLEFNLSLKLKDLTVGDTVMT 782

Qy 179 LMGIGSTLTDLTLNTGATTNVTNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTASD- 236

Db 783 TNGV-----TVSGVTLGSMGLVITDGPSVTSSTGI-----NAGSQKITNVAAGTADTDA 831

Qy 237 -----NVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKICAKTSV 280

Db 832 VNLSQLNTAMAGSGAKSVHYIYTD-----GGTQGGNYNGDGATGTRSIAGVGVTLASA 885

Qy 281 IKEKDGKLVTKDKGKENG-SSTDEGEGLVTAKEVIDAVNKAGWRMKT---TANGQTQADKF 339

Db 886 -----EGATAVSGSAAAASGKSTAIGRNAVASADGSVALGD-GAKDGAARGAESYTKYSGL 940

Qy 340 ETVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQL-----QNSGNWLDISK 395

Db 941 QNNTVGTVSVGDASKGETRVS-----NVADAKEAT--DAVNLQOLDRVAQDANRYVDNK 993

Qy 396 AVAGSSGKVISGNVSPSKGKMDETVINAGNNITETRNGKNIDTATSMTPQFSSVSLGAG 455

Db 994 IESLSEGQTF-----VKVNSLNN-----SATP-----IAAG 1019

Qy 456 ADAPTLVS-----DGDALNVGSK-----KDNKPV-----RITNV 484

Db 1020 VDATAIGVGATASGADSIAMGNKASASADNAVAIGNHVSADRANTVSVGSAGSERQVTNV 1079

Qy 485 APGVKEGDTVNTVAQLKGVQNLNNRIDNVGDNAR-----AGIAQAIATAGLVQAYLPCKSM 540

Db 1080 AAGTADTDVAVNVSQLNQGLITAKQYTDGVVGSLSLRDTDGGVAAAATATANLPQAYIPGRGM 1139

Qy 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGQYW 591

Db 1140 TSVGVSSYRGQSAIAVGVSSVSESGRWVFKFSANTRSQVIGAGVGQYW 1190

RESULT 7

A86036

probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: A86036

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A86036

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1588 <SPO>

A:Cross-references: GB:AE005174; NID:gl2518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5029

Query Match 12.1%; Score 363; DB 2; Length 1588;

Best Local Similarity 24.7%; Pred. NO. 3.1e-10;

Matches 145; Conservative 78; Mismatches 228; Indels 136; Gaps 22;

Qy 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGKNV-ITSDTKGLNFAKETAGTNGDTTVHL 179

Db 1022 NATNMMIEQNTQIINQLAGNTDATYIQENGAGINYVRTNDDGLAFNDASAOQVGATAIGY 1081

Qy 180 NGI-----GSTLTDTLLNTGA-TTNVTNDNV-----TDDE 208

Db 1082 NSVAKGDSSVAIGQGSYSDVDTGIALGSSSVSRVIAKGRDTSITENGVVIGYDITDGE 1141

Qy 209 KKRAASVKD-----VLNAGWNKGVKPGTTASDNDVFRVTYDVEFLSADTKTTVNVE 262

Db 1142 LLGALSIGDDCKYRQIIN-----VADGSEAHDAVT-VRQLQNAIGAVATTPTKYFHAN 1193

Qy 263 SKDNGK----KTEVKIGAKTSVIKEK-----DGKLVTKDKKE----- 296

Db 1194 STEEDSLAVGTDSLAMGAKTIIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVSIAI 1253

QY 297 -NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQ-----TGQADKFETVTSGTNV 348

Db 1254 GNGSTTRGAQTNYTAYNMDAPONSVEFSVGSADQQRQITNVAAGSAD-----TDAVNV 1308

QY 349 TFASGKGTATTATVSKDDQGNITVM-----YDVNVGDAL-----NVNQL 385

Db 1309 --GQLKVTDAQVSONTO-SITNLDNRVTNLDSTRVTNIENGIGDIVTTGSTKYFKTNTDGV 1365

QY 386 QNSGWNLDKAVAGSSGKVISGNVSPSKGKM---DET VNINAGNNIEITRN---GKN--- 436

Db 1366 DASAQKDSVAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNQRRITNVAAGKNATD 1425

QY 437 -IDIATSMTPQFSSVSLGAGADAPTLSDVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTN 495

Db 1426 AVNVAQLKSSEAGGVRYDTKADG---SIDYSNITLGG-GNGGTTTRISNVSAGVNNNDVNV 1481

QY 496 VAQLKGVAQ-----NLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPCSKSMMMAIG 544

Db 1482 YAQLKQSVQETKQYTDORMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIG 1541

QY 545 GGT YRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 591

Db 1542 GGT YNGESAVALGVS MV SANGRWVYK LQGSTNSQGEYS AALGAGIQW 1588

RESULT 8

H91188

probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001

C;Accession: H91188

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: H91188

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1588 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs4480

Query Match 12.1%; Score 363; DB 2; Length 1588;

Best Local Similarity 24.7%; Pred. No. 3.le-10;

Matches 145; Conservative 78; Mismatches 228; Indels 136; Gaps 22;

QY 121 NGTNFTYSLKKDLTLTSVGTEKLSF SANGKNV-ITSDTKGLNFAKETAGTNGDITVHL 179

Db 1022 NATNMMIEQNTQIINQLAGNTDATYIQENGAGINVRTNDGGLAFNDASAQGVGATAIGY 1081

QY 180 NCI-----GSTLTDTLNTGA-TTNVTNDV-----TDDE 208

Db 1082 NSVAKGDSSVAIGQGSYSDVDTGIALGSSSVSRVIAGKSRDTSITENGVVIGYDITDGE 1141

QY 209 KKRAASVKD-----VLNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTVNVE 262

Db 1142 LLGALSIGDDGKYRQIIN-----VADGSEAHDAVT-VRQLQNAIGAVATTPTKYFHAN 1193

QY 263 SKDNGK----KTEVKIGAKTSVIKEK-----DGKLVTKGDKGE----- 296

Db 1194 STEEDSLAVGTD SLAMGAKTIIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVSIAI 1253

QY 297 -NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQ-----TGQADKFETVTSGTNV 348

Db 1254 GNGSTTRGAQTNYTAYNMDAPONSVEFSVGSADQQRQITNVAAGSAD-----TDAVNV 1308

QY 349 TFASGKGTATTATVSKDDQGNITVM-----YDVNVGDAL-----NVNQL 385

Db 1309 --GQLKVTDAQVSONTO-SITNLDNRVTNLDSTRVTNIENGIGDIVTTGSTKYFKTNTDGV 1365

QY 386 QNSGWNLDKAVAGSSGKVISGNVSPSKGKM---DET VNINAGNNIEITRN---GKN--- 436

Db 1366 DASAQKDSVAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNQRRITNVAAGKNATD 1425

QY 437 -IDIATSMTPQFSSVSLGAGADAPTLSDVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTN 495

Db 1426 AVNVAQLKSSEAGGVRYDTKADG---SIDYSNITLGG-GNGGTTTRISNVSAGVNNNDVNV 1481

QY 496 VAQLKGVAQ-----NLNRRIDNVGDNARAGIAQAIAATAGLVQAYLPCSKSMMMAIG 544

Db 1482 YAQLKQSVQETKQYTDORMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIG 1541

QY 545 GGT YRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW 591

Db 1542 GGT YNGESAVALGVS MV SANGRWVYK LQGSTNSQGEYS AALGAGIQW 1588

RESULT 9

AH0110

probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C;Accession: AH0110

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0110

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-658 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175

C;Genetics:

A;Gene: YPO0902

Query Match 11.0%; Score 331.5; DB 2; Length 658;

Best Local Similarity 25.2%; Pred. No. 3.6e-09;

Matches 132; Conservative 74; Mismatches 204; Indels 113; Gaps 22;

QY 101 GVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTLTSVGTEKLSF SANGKNVNITSDTK 160

Db 217 GAVTSQANSIALG-AASINTVGAQSSYSAYALTAPQASVGELGIG-TALGNR-KITGVAA 273

QY 161 GLNFAKETAGTNGDITVHLNGIGSTLTDTLNTGATNVTN--DNVTDDEKKRAASVKDV 218

Db 274 G-----SASSDAVNVAQLTAVGDQVQQN-----TANITSLGGRVTTIE----GSMASI 317

QY 219 LNAGWNIKGVPKGT TASDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKKT-----EV 272

Db 318 ANGG-GVKYFHFANSTQPDV-----ASGTNSVAIGPASLASGNAALASGAGAV 364

QY 273 KIGAKTSVIKEKDGKLVTKDKKGENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQ 332

Db 365 AIG--DGAASADGSVAIGQSGDNGRGENYIG-----KYSNASNTS 405

QY 333 TGQADKFETVTSGTNVTFASGKGTATTATVSKDDQGNITVMYDVNVGDALNVNQLONGSWNL 392

Db 406 SG-----TVSVGNAT-----GETRTVSNVADG-----LQATDAVNLRLQD----- 442

QY 393 DSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNI-EITRNGKNIDI--ATSMTPQFSS 449

Db 443 -----IAASIVVVENNVSGLQNGTDMGFQVNNSSGLAKPSATGANSATGGAGSVASGNNS 497

QY 450 VSLGAGADAP-----TLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL 499

Db 498 TAFGSGAKATAANS AALGANSVADRANSVSGSVGNER-QITNVAPATQGTDAVNFQDL 555









Db 1236 --NGAEINATEGAATLTATGNTLTTEAGSS-----ITST-----KGQVDLLAQNGSIA 1281  
QY 504 QNLNNRIDNVGNARAGIAQAATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISD 563  
Db 1282 GSIN--AANVTLN-----TTG-----TLTTVAGSDIKATSG-----TLVIN 1315  
QY 564 GGNWIIKGTASGNS 577  
Db 1316 AKDAKLNGLDASGDS 1329  
RESULT 14  
C48399  
ABC-type transport protein ydbA.2 - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 19-Nov-1993 #sequence\_revision 16-Oct-1998 #text\_change 08-Oct-1999  
C:Accession: C48399; D64891; H64891  
R:Moszer, I.; Glaser, P.; Danchin, A.  
Biochimie 73, 1361-1374, 1991  
A:Title: Multiple IS insertion sequences near the replication terminus in Escherichia coli  
A:Reference number: A48399; MUID:92190338  
A:Accession: C48399  
A:Molecule type: DNA  
A:Residues: 464-2020 <MOS>  
A:Cross-references: GB:D85081; NID:g3041754  
A:Experimental source: strain K-12  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:88089, NCBIIP:88090)  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64891  
A:Molecule type: DNA  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Residues: 1-839, 'LDLPLYFQTSVIT' <BLA1>  
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g1787668;  
A:Experimental source: strain K-12, substrain MGL655  
A:Accession: H64891  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'M', 915-2020 <BLA2>  
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g1787672;  
A:Experimental source: strain K-12, substrain MGL655  
C:Genetics:  
A:Gene: ydbA\_2  
A:Start codon: GTG

Query Match 7.4%; Score 221; DB 2; Length 2020;  
Best Local Similarity 23.6%; Pred. No. 0.0041;  
Matches 167; Conservative 75; Mismatches 230; Indels 236; Gaps 40;  
QY 50 SANNEEQEEDLYLDPVQRTV----AVLIVNSDKEGT-----GEKEV-----EENS 92  
Db 141 SFNN-----DVLDKTEKTLTRDSVFTYTENADGTISLQDSNGRKATINLWQIDEANNT 195  
QY 93 WAV-----YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGT 141  
Db 196 VALEGVSADGATKWQYNHNGELVI-----TGDNATVNNNG-----KTTVDGKDSGT 242  
QY 142 E-----KLFSANGKNVNITSDT-----KG-----LNF 164  
Db 243 EINGNNGKVIQDGLDVSGGGHIDITGDSATVDNKGTMFTVDPESMGIQIDGDKAIVNN 302  
QY 165 AKETAGTNGDTTVHLNG-----IGSTLTDLTLNLTGATTVNTNDNVTDDEKKRAASVKD 217  
Db 303 EGESTITNGGTGTQINGDDATANNNGKTTVDGKDSGTGTENGNGKVIQD-----GDLD 356  
QY 218 VLNAGWNKIKGKPGTTASDNVDVVRTYDVEF-LSADTKTTTVNVESKD----- 265

Db 357 VSGGGHGI-DITGDSATVDNKGTMFTVTDPEISIGIQVDGDQAVVNNEGESAITNGTGTQI 415  
QY 266 NGKKEVKGIGAKTSVIKEKDGKLVTKD-KGENG-----SSTD 302  
Db 416 NGDDATANNGKTTV---DGKDSGTETIAGNNGKVIQDGLDVSGGGHIDITGDSATV 471  
QY 303 EGEGLVTAKE-----VIDA-----VNKAGWRMKTATTANGQTGQADKFETVTSGTNVTFAS 352  
Db 472 DNKGTMTVTDPEISIGIQIDGDAQIIVNEG---ESTITNGGTG-----TQINGNDAT-AN 521  
QY 353 GKGTATATVSKDD-----QGNITVYMDVNVGDALNV---NQLQNSGWN---LDSK-----A 396  
Db 522 NSGKTTVDGKDSGTGTKIAGNIGI---VNLGSLTVTGGAHGVENIGDNGTNNKGDIVVS 578  
QY 397 VAGSSGKVISGNVSPSKGKMDETVNNAGNNIEITRNKGKNIDATISM-TPQFS----- 448  
Db 579 DTGSIGVLINGEGATVSNVTGDVNVVS-NEATGFSITTSNGKVSLSAGSMQVGFSTGVDLNG 637  
QY 449 ---SVSLGA-----GADAPTLTSLVDGDALNV---GSKKDNKPKVITNVA-----PGV--- 488  
Db 638 NNNSVTAAKDLKVVVGQKATGINVSGDANTVNITGNVLVDKDKTADNAAEYFFDFPSVGIN 697  
QY 489 ---KEGDTNVAQLKGAQN-LNNRIDNV-DGNARAGIAQAATAGLV----- 531  
Db 698 VYGSDNNVTLDGKLTVVSDSEVTSRQSNLFDGSAE-----KTSGLVIGDGNVTNMNG 750  
QY 532 -QAYLPGKSMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIG 571  
Db 751 GLELIGEKNALADGSQVTSRLRTGYSTVSVIVVSGESSVYLNGBDTTISG 798  
RESULT 15  
AF0394  
probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0394  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175  
C:Genetics:  
A:Gene: hmwA

Query Match 7.3%; Score 219; DB 2; Length 1910;  
Best Local Similarity 20.5%; Pred. No. 0.0048;  
Matches 148; Conservative 92; Mismatches 255; Indels 228; Gaps 28;  
QY 14 NAWVAVSELTRNHTKRASATVKTAVLATLLFATVQ-----ASA 51  
Db 898 NATITANNISMN---GNITANDAVLMTNFTLTAKGDIKTDLTSPTKGLWFRNGGMTAA 953  
QY 52 NNEEQEEDLYDPVQRTVAVLIIVNSDKEGTGEKEKVEENSMDWAVYFNEKGVLTAREITLK 111  
Db 954 NN-----ILLVANS--TSSGETVKINASSS-----NKMNITACKDISII 990  
QY 112 AG-----DNLKIKONGTNFTYSLKKDLTDLTSVGTSEKLSFSANGKNVNITS 159  
Db 991 AGNSKTATGPNINIENVNIENTNNGNFT-----TNGITSTWLSGVNVSANG---VDITSNS 1042  
QY 160 KGLNFAKETAGTNGDTTVHLNGIGSTLTDLTLNLTGATTVNTNDNVTDDEKKRAASVKDV- 218  
Db 1043 TG-----TGGIVLDNTNLTITVGD-----INT-IVTNSSGKGIWIKSNSTLNSNKDIT 1089  
QY 219 ---LNAGWNKIKGV--KPGTTASDNVDVVRTYDVEFLSADTKTTTVNVESKDNKKKEVK 273

Db 1090 LVGVSAGQN-EGVIIQSSDASRN-----NISAQGNITLIGKMGSGQHSLIN 1137  
QY 274 IG--AKTSVIKEKDGLVTKDKGKENGSSSTDEGLVTAKEVIDAVNKAGWRMKTSTA-- 329  
Db 1138 LGNVSLS-----SGRNIDINGSSAGTGDVYFTNVELNATAGNVSIIAETKTALS 1187  
QY 330 -----NGQTGOADKFFETVTSNTVTFASCKGTTATVSKDDQGNITV----- 370  
Db 1188 TSLNAVLSLGGNNSIKAQNGWLIGKAFNTTQAGIGIFRANSSLSVDGNIILKGETEGVGA 1247  
QY 371 -----MYDVNVGDALNVNQLNSGWNLDSKAVAG----- 399  
Db 1248 TRKGIDFYGANTLIIKGSQSLGKQADTAGGNGISYTSIAKLTVNNNGSLKMEGR 1307  
QY 400 -----SSGKVISGNVSPSKGMD----- 417  
Db 1308 STSGTGINFPPSSNNTLVFNGDGTLLIKGSSVAGTGAISGVVNNSTGPMTEIGISTDGAG 1367  
QY 418 -----ETVNINAGN---NIEITRNGKNIDIA-TSMTPOFSSVSLGA--GADAPT 460  
Db 1368 VHLFSAEHRIDRINTGSSSTHAEGLRISGNAIIVDTTLTGKSINGSGVKIDSLPGSSVVT 1427  
QY 461 LSVGDGALNVGSKDKNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNIDNVNVDGNARAG 520  
Db 1428 RSVLDNATLNGSSSSGKGVEITSDINGIIHSSINGTTGTGYGIDIGEN-SNVGTSEAD 1486  
QY 521 --IAQAIATAGL-VQAYLPKSMMAIGGGTYRGEAGYAIGYSS-ISDGGNWIIGKTASGN 576  
Db 1487 LLLIQGVATTGTGTGIKLNGNNDLSNTSLNSSAVDGIALDITGPLANQGNVILNGTASGS 1546  
QY 577 SRG 579  
Db 1547 GIG 1549

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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:31:01 ; Search time 19.11 Seconds  
(without alignments)  
1197.449 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVG YQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	235.5	7.8	1039	1 AG43_ECOLI	P39180 escherichia
2	221	7.4	2003	1 YDBA_ECOLI	P33666 escherichia
3	212.5	7.1	1286	1 AIDA_ECOLI	Q03155 escherichia
4	210	7.0	1325	1 YDEK_ECOLI	P32051 escherichia
5	207.5	6.9	1577	1 HLYA_PROMI	P16466 proteus mir
6	201	6.7	1654	1 OMPB_RICRI	Q53047 r outer mem
7	191.5	6.4	1608	1 HLYA_SERNA	P15320 serrattia ma
8	191	6.4	2249	1 OMPA_RICRI	P15921 rickettsia
9	189.5	6.3	1953	1 BIGA_SALTY	P25927 salmonella
10	186.5	6.2	1655	1 OMPB_RICCN	Q9kka3 r outer mem
11	185	6.2	1645	1 OMPB_RICTY	P96989 r outer mem
12	183	6.1	1007	1 Y741_CHLMU	Q9pjt6 chlamydia m
13	182	6.1	917	1 HXA3_HAEIN	P45355 haemophilus
14	181	6.0	1656	1 OMPB_RICJA	O06653 r outer mem
15	180.5	6.0	928	1 HXA2_HAEIN	P45354 haemophilus
16	180.5	6.0	933	1 SLAP_CAMFE	P35827 campylobact
17	180.5	6.0	1569	1 YPJA_ECOLI	P52143 escherichia
18	180	6.0	2334	1 WAPA_BACSU	Q07833 bacillus su
19	176	5.9	1861	1 APU_THETU	P38536 t amylopull
20	175.5	5.8	1567	1 ICEN_XANCT	P18127 xanthomonas
21	175	5.8	2021	1 OMPA_RICCN	Q52657 rickettsia
22	174	5.8	918	1 YMJB_CAEEL	P34487 caenorhabdi
23	167.5	5.6	1148	1 ICEK_PSESX	O30611 pseudomonas
24	167	5.6	1643	1 OMPB_RICPR	Q53020 r outer mem
25	166	5.5	1025	1 SLAP_CAUCR	P35828 caulobacter
26	165.5	5.5	1300	1 120K_RICRI	P14914 rickettsia
27	164.5	5.5	444	1 SLAP_LACAC	P35829 lactobacill
28	163	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
29	161.5	5.4	1637	1 MRSP_STAAU	P80544 staphylococ
30	159.5	5.3	642	1 FLID_CAMJE	Q9phw6 campylobact
31	159	5.3	671	1 ALYS_ENTFA	P37710 enterococcu
32	159	5.3	928	1 PM10_CHLPN	Q9rb65 chlamydia p
33	158	5.3	497	1 FLIC_ECOLI	P04949 escherichia

ALIGNMENTS

RESULT 1					
AG43_ECOLI					
ID AG43_ECOLI	STANDARD;	PRT;	1039 AA.		
AC P39180;	P76360;	P75614;	P97241;	Q46771;	P44969 haemophilus
DT 01-FEB-1995	(Rel. 31, Created)				P45384 haemophilus
DT 01-NOV-1997	(Rel. 35, Last sequence update)				P50493 plasmodium
DT 16-OCT-2001	(Rel. 40, Last annotation update)				O33479 pseudomonas
DE Antigen 43 precursor (AG43) (Fluffing protein).					P46949 saccharomyc
GN FLU OR B2000.					P06620 pseudomonas
OS Escherichia coli.					P20676 saccharomyc
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;					Q06974 salmonella
OC Escherichia.					P56867 deinococcus
OX NCBI_TaxID=562;					P15345 caulobacter
RN [1]					Q92kw5 helicobacte
RP SEQUENCE FROM N.A.					P46590 candida alb
RC STRAIN=K12 / MGL655;					
RX MEDLINE=97426617; PubMed=9278503;					
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,					
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,					
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,					
RA Mau B., Shao Y.;					
RT "The complete genome sequence of Escherichia coli K-12.";					
RL Science 277:1453-1474(1997).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC STRAIN=K12;					
RX MEDLINE=97251358; PubMed=9097040;					
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,					
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,					
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,					
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,					
RA Sivasubdaram S., Tagami H., Takeda J., Takemoto K., Wada C.,					
RA Yamamoto Y., Horluchi T.;					
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome					
corresponding to the 40.1-50.0 min region on the linkage map.";					
RL DNA Res. 3:379-392(1996).					
RN [3]					
RP SEQUENCE FROM N.A.					
RC STRAIN=ML 308-225;					
RA Henderson I.R., Owen P.;					
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.					
RN [4]					
RP PRELIMINARY SEQUENCE OF 53-78.					
RC STRAIN=ML 308-225;					
RX MEDLINE=89291704; PubMed=2661530;					
RA Caffrey P., Owen P.;					
RT "Purification and N-terminal sequence of the alpha subunit of antigen					
43, a unique protein complex associated with the outer membrane of					
Escherichia coli.";					
RL J. Bacteriol. 171:3634-3640(1989).					
RN [5]					
RP SEQUENCE OF 53-63.					
RC STRAIN=K12 / EMG2;					
RX MEDLINE=97443975; PubMed=9298646;					
RA Link A.J., Robison K., Church G.M.;					
RT "Comparing the predicted and observed properties of proteins encoded					



RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 464-2003 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92190338; PubMed=1665988;  
RA Moszer I., Glaser P., Danchin A.;  
RT "Multiple IS insertion sequences near the replication terminus in  
RL Escherichia coli K-12.";  
RL Biochimie 73:1361-1374(1991).  
CC -!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).  
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR  
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
CC BETWEEN AMINO ACIDS 839 AND 840.  
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CC -----  
DR EMBL; AE000237; AAC74483.1; ALT\_SEQ.  
DR EMBL; AE000237; AAC74487.1; ALT\_SEQ.  
DR EMBL; D90778; BAA15009.1; ALT\_SEQ.  
DR EMBL; D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL; D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL; X62680; -; NOT\_ANNOTATED\_CDS.  
DR EcoGene; EG11307; ydba.  
KW Hypothetical protein; Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;  
  
Query Match 7.4%; Score 221; DB 1; Length 2003;  
Best Local Similarity 23.6%; Pred. No. 0.0015;  
Matches 167; Conservative 75; Mismatches 230; Indels 236; Gaps 40;  
  
QY 50 SANNEEQEEDLYLDPQRTV---AVLIVNSDKRGKT-----GEKEKV-----EENSND 92  
Db 141 SFNN----DVILDKTEKTLTIRDSVFYTYTENADGTISLQDSNGRKATINLWQIDEANNT 195  
  
QY 93 WAV-----YFNEKGVLTAIREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGT 141  
Db 196 VALEGVSAADGATKWQYNHNGELVI-----TGDNATVNNNG-----KTTVDGKDSTGT 242  
  
QY 142 E-----KLSEFANGKNVNITSDT-----KG-----LNFF 164  
Db 243 EINGNNGKVIQDGLDVSGGGHGIDITIGDSATVDNKGTMVTDPESMGIQIDGDKAIVNN 302  
  
QY 165 AKETAGTNGDTTVHLNG-----IGSTLTDTLLNTGATTNVTNDNVTDDKKRAASVKD 217  
Db 303 EGESTITNGGTGTQINGDDATANNNGKTTVDGKDSTGTTEINGNNGKVIQD-----GDLD 356  
  
QY 218 VLNAGWNIKGVPKGTASDNVDFVRTYDTVEF-LSADTKTTTVNVESKD----- 265  
Db 357 VSGGGHGI-DITGDSATVDNKGTMVTDPEISIGIQVDGDQAVWNNEGESAITNGGTGTQI 415  
  
QY 266 NGKKEVTEVIGAKTSVIKEKDKGLVTGKD-KGENG-----SSTD 302  
Db 416 NGDDATANNNGKTTV-----DGKDSTGTETIAGNNGKVIQDGLDVSGGGHGIDITGDSATV 471  
  
QY 303 EGEGLVTAKE-----VIDA-----VNKAGWRMKTATTANGQTQADKFFETVSGTNVTFAS 352  
Db 472 DNKGTMTVTDPEISIGIQIDGDAQAIVNNEG---ESTITNGGTG-----TQINGNDAT-AN 521  
  
QY 353 GKGTATATVSKDD-----QGNITVMYDVNVGDALNV-----NLQNSGWN--LDSK-----A 396  
Db 522 NSGKTTVDGKDSTGKTIAGNIGI---VNLDGSLTVTGGAHGVENIGDNGTVNKNKGDIIVS 578  
  
QY 397 VAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKGKNIDIATSM-TPQFS----- 448  
Db 141 SDWAVYFNEKGVLTAREIT-----LKAGDNLKIKQNGTNFTYSLK-KDLTDLTSVGT 141

Db 579 DTGSIGVLINGEGATVSNNTGDVNVVS-NEATGFSITNSGKVLASGSMQVGFSTGVLDLNG 637  
QY 449 ---SVSLGA-----GADAPTLSDVDGALNV---GSKKDNKPVRIITNVA-----PGV--- 488  
Db 638 NNNSVTAAKDLKVVGOKATGINVSGDANTVNITGNVLVDKDKTADNAAEYFDPSPVGIN 697  
QY 489 ---KEGDTVNVQQLKGVAQN-LNNRIDNV-DGNARAGIAQAIAATAGLV----- 531  
Db 698 VYGSDNNVTLDGKLTVVSDSEVTSRQSNLFDGSAE-----KTSGLVVGIDGNTVNMNG 750  
QY 532 -QAYLPKGSMMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIGK 571  
Db 751 GLELIGEKNALADGSQVTSRLTGYSTYSVIVVSESSVYVLNGDTTISG 798  
  
RESULT 3  
AIDA\_ECOLI  
ID AIDA\_ECOLI STANDARD; PRT; 1286 AA.  
AC Q03155;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Adhesin aida-I precursor.  
GN AIDA-I.  
OS Escherichia coli.  
OG Plasmid pIB6.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.  
RC STRAIN=2787 (O126:H27);  
RX MEDLINE=92326638; PubMed=1625582;  
RA Benz I., Schmidt M.A.;  
RT "AIDA-I, the adhesin involved in diffuse adherence of the  
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is  
RT synthesized via a precursor molecule.";  
RL Mol. Microbiol. 6:1539-1546(1992).  
CC -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE  
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI  
CC TO EPITHELIAL CELLS.  
CC -!- SUBCELLULAR LOCATION: Outer membrane.  
CC -----  
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CC -----  
CC EMBL; X65022; CAA46156.1; -.  
DR PIR; S28634; S28634.  
KW Cell adhesion; Signal; Outer membrane; Plasmid.  
FT SIGNAL 1 49  
FT CHAIN 50 ? ADHESIN AIDA-I.  
FT PROPEP ? 1286  
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;  
  
Query Match 7.1%; Score 212.5; DB 1; Length 1286;  
Best Local Similarity 21.1%; Pred. No. 0.0023;  
Matches 144; Conservative 94; Mismatches 274; Indels 171; Gaps 29;  
  
QY 1 MNKIYRIIWNALNAWVAVSELTRNH-----TKRASATVKTA--VLATLLEATVQASA 51  
Db 1 MNKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFVAVNISGTVSSGG 60  
  
QY 52 NNEEQEEDL-----YLDPVQRTVAVLIVNSDKEGTGEKEKVEE---N 90  
Db 61 TVSSGETQIVYSGRGNATVNSGGTQIVNNGGKTTATTVNSSGSGQNVGTSGATISTIVN 120  
  
QY 91 SDWAVYFNEKGVLTAREIT-----LKAGDNLKIKQNGTNFTYSLK-KDLTDLTSVGT 141



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Db 121 SGGTQVSSGGVASATNLSGGAQNIYNLGHASNTVIFSGNQITFSGGITDSTNISSGQ 180
QY 142 EKLSFSANGKVNITSDTKGLNFAKETAGTNGDITVHLN-----GIGSTLTDTLNTG 194
Db 181 QRV--SSGGVASNTTINSSG---AQNILSEGAISTHISGGNQYISAGANATETIVNSG 235
QY 195 ATTNVTNDNVTDDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDVFTVYDVEFLSADT 254
Db 236 GFORVNSG-----AVATGTVLSSG--TQNVSSGGSAISTSVYNSGVQTV-FAGATV 283
QY 255 KTTTVNVEKDN---GKKTEYKIGAKTSVKEKDGKLVTKDKKGNGSSTDEGEGLVTA 310
Db 284 TDTTVNSGGNQNISSGGIVSETTVNSGTVNQNIYSSGGSALSANIKGS----- 329
QY 311 KEVIDAVNKAGWRMKTITANG-----QTGOADKFFETVTSCTNVTFASG-----KGT 356
Db 330 ---QIVNSEGTAINTLVSDGQYQHIRNGGFIASGTIVNQSGYVNVISGGYAEISTIINSG 385
QY 357 TATVSKDDQGNITVMYD---VNVGD-ALNVNQLQNSGWNL-----DSKAVAGSSG--K 403
Db 386 TLRVLSGARGITLNSGRENVSNGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQR 445
QY 404 VTSGNVSPSKAMDETVNIAGN---NIEITRNGKN-----IDIATSMTPQF 447
Db 446 INSGGTAPQVNSVVVTRTVSSAAKPFDAEYVSGGKQTVLWRGIWISNFLTAVWSMFPCT 505
QY 448 SS---VSLGAGADAPTLSVDGDALN-----VGSKKDNKPVRIITNVAPGV 488
Db 506 ASGANVNLSGRLNAFAGNVVGTILNQEGROYVYSGATATSTVGNNEGREV---LSGGI 561
QY 489 KEGDVTNVAQLKGVAQNLLNNRIDNVGDNARA-----GIAQAIATAGLVQAYLPKSKMMAI 543
Db 562 TDGTVLNSGGGLQAVSSG-----GKASATVINEGGAQFVYDGGQV-----TGCTNIK-- 606
QY 544 GGGTYRGEAGYAGYSSISDGCN 566
Db 607 NGGTIRVDSGASALNIALSSGGN 629

RESULT 4
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORET).
GN YDEK OR ORET OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
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RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Litchgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
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CC -----
CC EMBL; AE000248; AAC74583.1; -
CC EMBL; D90793; BAA15190.1; ALT_INIT.
CC EMBL; D90794; BAA15197.1; ALT_INIT.
CC EMBL; X73295; CAA51730.1; ALT_FRAME.
CC PIR; S34315; S34315.
CC EcoGene; EG11780; ydek.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC Hypothetical protein; Membrane; Lipoprotein; Signal;
CC Complete proteome.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
CC LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
CC CONFLICT 884 884 N -> K (IN REF. 3).
CC CONFLICT 1317 1317 M -> S (IN REF. 3).
CC SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;
DR -----
DR EMBL; AE000248; AAC74583.1; -
DR EMBL; D90793; BAA15190.1; ALT_INIT.
DR EMBL; D90794; BAA15197.1; ALT_INIT.
DR EMBL; X73295; CAA51730.1; ALT_FRAME.
DR PIR; S34315; S34315.
DR EcoGene; EG11780; ydek.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 7.0%; Score 210; DB 1; Length 1325;
Best Local Similarity 22.9%; Pred. No. 0.0032;
Matches 148; Conservative 72; Mismatches 266; Indels 160; Gaps 27;

QY 1 MNKIYRIIWNALNVAWVAVSELTRNTHKRASATVKTAVLATLFLFATVQASANNEEEEDL 60
Db 1 MNRIYRVINWCTLQVFQACSELTRRAGKTSTVNLKSSGLTTKFSRL----- 47
QY 61 YLDPVQRTVAVLIVNSDKKEGTEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
Db 48 -----TLGVLLALS---GSASGASLEVDNDQI----- 71
QY 121 NGTNFTYSLKKDLTDLTSVGTKEKLSFSANGKNVNITSDTKGLNFAKETAGTNGDITVHLN 180
Db 72 --TNIDTDVAYDAYLVGWYGTGVNLILAGGN-ASLTITTSV-----IGANEDSEGTVN 122
QY 181 GIGST--LTDT-----LLNTG----ATTNVTNDNVTDDDEKKRAASVKDVLNAGWNKGVK 229
Db 123 VLGGTWRLYDSGNNARPLNVGQSGTGTNLNIKQKHVDG-----GYLRIGSSTGGV- 172
QY 230 PGTTASDNVDFVRTYDVEFLSADTKTTTVNVEKDKGKKTE-----VKIGAKTSVIK 282
Db 173 -GTNVVEGDSVLTTELFEGISYGTGSLNIT---DKGYVTSSIVAILGYAGSNQVVV 227
QY 283 EKDGK-LVTGKDKG-----ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQT 333
Db 228 EKGGEWLIIKNNDSSIEFFIGNQGTGEATIREGGLVTAENTIIIGNATG----IGTLNVQ- 282
QY 334 GQADKFETVTSNTVTFASGKGTTATVTSKDDQGNITVMYDVNVGDALN--VNLQNSGWN 391
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Db 283 -DQDSVITVRRLYNGYFGNG---TVNISNNGLINNKKEYSLVGVDGSGHGVNVNTDKGHN 338
QY 392 L-----DSKAVAGSSGKVISGNVSPSKGKMDET-----VNIN 423
Db 339 FLGTGEAFRIYICDAGDGLNLSSEKGVDSGIITAG---MKETGTGNTIVKDKNSVITN 395
QY 424 AGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKD-NKPVRIT 482
Db 396 LGTNLGYDGHGEMNISQGLVVSNGSSSLGYG-----ETGVGNVSITTGGMWEVKNVYTT 451
QY 483 NVAPGVKEGVTNVQAQLKGVAQNLRIDNVGDNARAGIAQAIATAGLVQAYLP--GKSM 540
Db 452 IGAVGVGNLNISDGG--KFVSNITFLGDKASGIGTGLNLMDATSSFTVGINVGNFGSGI 509
QY 541 MAIGGGTYRGEAGYAI-----GYSSISDGGNWIIGKTASGNSR 578
Db 510 VNVSGATLNSTGYGFIGGNASGKGIVNISDLSLWNLK-TSSTNAQ 554

RESULT 5
HLVA_PROMI
ID HLVA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
CC REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
```

Query Match 6.9%; Score 207.5; DB 1; Length 1577;  
Best Local Similarity 22.3%; Pred. No. 0.0052;  
Matches 154; Conservative 86; Mismatches 258; Indels 193; Gaps 32;

```
QY 22 LTRNHTKRASATVKTAVALATLLFATVQASANNEQEDLYLDPVQRTVAVLIVNSDK--- 78
Db 306 ITVNSGSSQTLTKTELKGNI--TLVASSHNQIKASDLMGDDITLQGADLTIDGKQLQQ 363
QY 79 -----EGTGEKEKVE-----ENSDWAVYFNEKGVLTAREITLKAGDNLK 117
Db 364 KETDIDNRWFYSWKYDVTKKEQIQIGSQIDAKNNATLTATKGDVTLDAAKINAGNNLA 423
QY 118 IKONGTNFTYSLKKDLTDLTSVG-TEKLSFSANGKNVITS-----DTKGLNFA 165
Db 424 INAN-----KDIHINGLVEKESRSENGKNRHNHTSRLESGWSNSHOTELKAS 471
QY 166 KETAG-----TNGDTTVHLN-----GIGSTLTDLTLL---NT 193
Db 472 ELTAGKDLGLDAQGSITAQGAKLHANENVLVNAKNINLVQKTNNDKTVTNDNHVMWGGI 531
QY 194 GATTNVTNDN-----VTDDEKKRAASVKDVLNAGWNIKG-----VKPGTASDNVD 239
Db 532 GGGQKNNNNQOVSHATQLTADGQLLLAADNNVNITGSQVKGNGQAFVK--TTQGDVVI 589
QY 240 FVRTYDTVEFLSAD-----TKTTTVNVESKDNKKTEVKIGAKTSVIKEKD-----GKL 288
Db 590 DNALSETISKIDERTGTAFAFNITKSSHKNETNKQTSGLSELISDAQLTVVSGNDVNVIGSL 649
QY 289 VTGKDK-----GE-NGSST-----DEGEGLVT---AKEVIDAVNKAGWRMKTITANG 331
Db 650 IKSADKLGIHSLGDINVKSAQQVTKIDDEKTSLAITGHAKEVEDKQYSAGFHITHTNKN 709
QY 332 QTGOADKFETVTSGTNVTFASGKGTTATVS--KDDQGNITVMYDVNVGDALNVNQLQNSG 389
Db 710 TSTETEQANSTISGANVDLQANKDVTTFAGSDLKTTAGNASITGD-NVAFVSTENKKQTD- 767
QY 390 WNLDISKAVAGSSGKVISGNVSPSKGMDETVYNINAGNNIEITRN-GKNIDIASMTPOFS 448
Db 768 -NTDTTISGGFS---YTGVDKVGSKADFOYD-KOHTQTEVTKNRGSOQTEVAGDLTITAN 822
QY 449 SVSLGAGA-----DAPTLSDVDGDALNVGSKKD-----NKPV 479
Db 823 KDLLHEGASHHVEGRYQESGENIQHLAVNDSETSKT--DSLNVGIDVGVNLDYSGVTKPV 880
QY 480 R-----ITNVAPGVKEGDTVNVQAQLKGVAQNLRIDNVGDNARAGIAQAIATAGLVQA 533
Db 881 KKAIEDGVNTTKPG-NNTDLTKKVTARDAIANLAN-LSNLE-TPNVGVEVGIK----- 930
QY 534 YLPGKSMMAIGGGTYRGEAGYAGYSSISDG 564
Db 931 -----GGGSQQSQTDSDQAVSTSINAG 951

RESULT 6
OMPB_RICRI
ID OMPB_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
```



```
Db 520 IQVGVOQTANAKAVRDDKTSWG-----GIGGGDN---K 549
QY 121 NGTNFTYSLKKDL---TDLTSVGTEKLSFSANGK-VNIT-SDTKGLNFAKETAGTNGDT 175
Db 550 NNSN-----RREISHASELTSGGTLRL---NGQQGVITGSKARGQKGGEVTA-THGGL 599
QY 176 TVHLNGIGSTLTDLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTAS 235
Db 600 RID-NALSTTVDKIDARTGTAFNITSSSHKADNSYQSSTASEL-----KSD 644
QY 236 DNVDFVRTYDVEF-----LSADTKTTTVNVE----- 262
Db 645 TNLTLVSHKDADVIGSQVASGGELSVESTGNINVKAAERQONIDEQKALTAVNGYAKEA 704
QY 263 -----SKDNGKKTEVKIGAKTSVKEKDGKLVGKDKGENGSS--TDEGEGL 307
Db 705 GDKQYRAGLRIEHTRDSEKTRTNSA--SSLGGSVKLLKAEKDVTFSGSKLVADKGDAS 762
QY 308 VTAKEV--IDAVNKAGWRMKTTTANG---QTGOADKFETVTSGTNVTFASGKGTTATVSK 362
Db 763 VSGNKVSFLAADDKTASNTTEQTKIGGGFYTGIDK---LGSVGEAGYENNK-TQAQSSK 818
QY 363 -----DDQGNITVMYDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGKM 416
Db 819 AITSGSDVKGNLT-----INARDKLTQOGAQSVCAGAYQENAAAGVDHLAAADTASTTTKT 874
QY 417 DETVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGA-----GADAPTLSDV 464
Db 875 DVGVNI-----GANVDYSAVTRPVERAVGKAAKLDATGVINDIGGIGAPNVGLD 923
QY 465 GDALNVGSKK--DNKPVRIITNVAPGV---KEGDV---TNVAQLKGVAQNLN----- 507
Db 924 IGAQGSSEKSRSSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKG-AVNLTADSHRSE 982
QY 508 ---NRIDNVDGNARAGIAQAIATAGLVQAYLPKSKMMAIG---GGTYRGEAGYAGYSS 560
Db 983 AAANRQDEQSRDTR-----GSAG-VRVYTTTGSDLTVDKAGEGGTQRSNSSASQAVTG 1034
QY 561 ISDGGNW-----IIKGTASGNSRGHFGASA 585
Db 1035 SIDAANGINNVKKDAIYQGTALNGGRGKTAVNA 1068
RESULT 8
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSTIAE OMPA/OMPB FAMILY.
CC
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CC -----
DR EMBL; M31227; AAA26380.1; -.
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.4%; Score 191; DB 1; Length 2249;
Best Local Similarity 24.4%; Pred. No. 0.051;
Matches 142; Conservative 56; Mismatches 212; Indels 172; Gaps 30;

QY 98 NEKGVLTAREITLKAGDNLKIKONGTNTFTYSLKK---DLTDLTSVGTEKLSFSAN-----G 150
Db 766 NANAVLTGAIDNTTGGDNVGV---LNLNGALSQVTGDIGNTNSLAT--ISVGAGTATLG 819
QY 151 NKVNITSDTKGLNFAKETAGTN-----GDF--TVHLNGIGSTLTDLLNT- 193
Db 820 GAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNVGVNLNLNGALSQVTGDIGNTN 879
QY 194 -----GATNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTASDNV 238
Db 880 SLATISVGAGTATLGGAVIKATTTKLTN-----AASVLTLTNANAVLTGAIDNTTGGDNV 934
QY 239 DVRTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVGKDKGENG 298
Db 935 GVLNLNGALSQVTGDIGNT-----NSLAT-ISVGAGTATL----- 968
QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGOADKFETVTSGTNVTFASGKGTTA 358
Db 969 -----GGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGI-VTFTGNSTVTG 1020
QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDISKAVAGSSGKVISGNVSPSKGMDE 418
Db 1021 NV-----GNTNALATVNVGAGL--LQVQGGVVKANTINLTDNASAVFTNPVVVTGAIDN 1073
QY 419 TVNINAG-----NNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGDL--NVG 471
Db 1074 TGNANNGIVTFTGNSTVTGNVGN-----TNALATVNVGAG---LLQVQGGVVVKANTI 1122
QY 472 SKKDN-KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGNARA---GIAQAIA 526
Db 1123 NLTDNASAVFTTN--PVVVTGAIDNTG-----NANNGIVTFTGNSTVTGDIGNTNALA 1173
QY 527 T-----AGL-VQAYLPKSKMMA-----IGGGTYRGEAGYAGY---SSIS 562
Db 1174 TVNVGAGITLQA---GGSLAANNIDFGARSTLEFNGLDGG-----GKAIPYFFKGAIA 1224
QY 563 DGGNWIHK-----GTASGNSRGH---FGASASVG 588
```



Db 1225 NGNNAILNVNTKLLTASHLTIGTVAEINIGAGNLEFIDASVG 1266

RESULT 9  
BIGA\_SALTY STANDARD; PRT; 1953 AA.  
AC P25927; P25928; Q9XCQ3;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Putative surface-exposed virulence protein bigA precursor.  
GN BIGA OR STM3478.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=602;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=14028;  
RA Stojiljkovic I., Valentine P., Heffron F.;  
RT "Salmonella typhimurium rhs homolog.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2.";  
RL Nature 413:852-856(2001).  
RN [3]  
RP SEQUENCE OF 1-765 FROM N.A.  
RC STRAIN=LT2;  
RX MEDLINE=91100301; PubMed=1987123;  
RA Wu J.Y., Siegel L.M., Kredich N.M.;  
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
RT requirement for a cloned cysg plasmid to overcome limiting siroheme  
RT cofactor.";  
RL J. Bacteriol. 173:325-333(1991).  
CC -! CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
CC in positions 414 and 732.

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CC -----  
DR EMBL; AF133696; AAD39458.1; -.  
DR EMBL; AE008859; AAL22340.1; -.  
DR EMBL; M64606; AAA27042.1; ALT\_FRAME.  
DR EMBL; M64606; AAA27043.1; ALT\_FRAME.  
DR PIR; C39200; C39200.  
DR PIR; D39200; D39200.  
DR StyGene; SGI0437; bigA.  
KW Virulence; Repeat; Signal; Complete proteome.

FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 1953 PUTATIVE SURFACE-EXPOSED VIRULENCE  
FT DOMAIN 101 252 PROTEIN BIGA.  
FT REPEAT 101 103 15 X 11 AA TANDEM REPEATS.  
FT REPEAT 104 113 1 (INCOMPLETE).  
FT REPEAT 114 122 2 (INCOMPLETE).  
FT REPEAT 123 133 3 (INCOMPLETE).  
FT REPEAT 134 144 4.  
FT REPEAT 145 155 5.  
FT REPEAT 155 155 6.

FT REPEAT 156 166 7.  
FT REPEAT 167 177 8.  
FT REPEAT 178 188 9.  
FT REPEAT 189 199 10.  
FT REPEAT 200 210 11.  
FT REPEAT 211 221 12.  
FT REPEAT 222 232 13.  
FT REPEAT 233 243 14.  
FT REPEAT 244 252 15 (INCOMPLETE).  
FT CONFLICT 207 207 D -> DRGDDVTPPDD (IN REF. 1).  
FT CONFLICT 514 514 A -> R (IN REF. 3).  
FT CONFLICT 1698 1698 D -> N (IN REF. 1).  
FT CONFLICT 1795 1798 QYLE -> ITLQ (IN REF. 1).  
FT CONFLICT 1836 1837 SA -> T (IN REF. 1).  
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match 6.3%; Score 189.5; DB 1; Length 1953;  
Best Local Similarity 23.1%; Pred. No. 0.051;  
Matches 126; Conservative 64; Mismatches 194; Indels 161; Gaps 29;

QY 113 GDNLIKQNGTNYSLKKDLTSLVSGTEKLSFSAANGKVNITSDTKGLNFAKETAGTN 172  
Db 447 GDNATIKNTGTS-----DISGAGSTGT-----VIDGNARVNND----- 480  
QY 173 GDTVHLNGIGSTLT-DTLL--NTGATT-----NVTNDNVTDDEKKRAASVKDVLN 220  
Db 481 GDMITDGGTGGHITGDNVIDNAGSTTVSGADATALYIEGDNAL-----VIN 528  
QY 221 AG-WNIKGVKPGITASDNVDFVRTYDTVEFLSADTKTTTVNVEKDKNGKKEVIGAKTS 279  
Db 529 EGNQTSISGGAAGTRIDGD-----DAHTTNTGDIADVAGSAAVII----- 568  
QY 280 VIKEDGKLVTKGDKGENGSTDEGEGLVT--AKEVI--DAVNKAGWRMKTITANGQTGQ 335  
Db 569 -----NGDNGSLTQAGDLLVTDGAMGIIYGTGNEA-----KNTGNATVRD 609  
QY 336 ADKFETVTSCTNVTF-----ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLONS 388  
Db 610 ADSVGFVVAGEKNTFKNGKDIDVSLNGTGALVS-GDMSQVTLGDGINV--VSVQDSEGV 665  
QY 389 GWNLDKAVAGSSGKV-ISGNVSPS-----KGKMDETVNNAGNNEITRNGK-NI 437  
Db 666 FSSATGVSVDGSDNAVDITGNVNISADYQDDLAAGAPPLTGVVVGNGNTVTNLGALNI 725  
QY 438 ---DIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNPVRIITNVAPGVKEGDTV 494  
Db 726 DDNDLSATGGQYLDVVGLSVTGDNDNVEIDG-GINTHSED--PLDGT-----ADIT 775  
QY 495 NVAQLKGVAQNLRNIDNVGNARAG----IAQAIATAGLV-----QAYLP---- 536  
Db 776 GISVSGNSTVTLNHG-STIDTNTVYGGHVVLARVNNNGSLILGDDSVVDVNVSYIPTGY 834  
QY 537 --GKSMMAIGGTYRGEAG-----YAI-----GYSSISDGGNWIKGTASGNSRGHFGA 583  
Db 835 TYNALLMADGEGTSIENKGDITSHGVYSVIRADNGSEVNSGDIILVYATSSNSSEDRAAI 894  
QY 584 SASVG 588  
Db 895 TRASG 899

RESULT 10  
OMPBL\_RICCN STANDARD; PRT; 1655 AA.  
ID OMPBL\_RICCN  
AC Q9KKA3; Q9KK98; Q9XC45;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].







```
DR EMBL; AE002342; AAF39550.1; -.
DR TIGR; TC0741; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 51 POTENTIAL.
FT CHAIN 52 1007 HYPOTHETICAL PROTEIN TC0741.
SQ SEQUENCE 1007 AA; 104006 MW; 842800C0871B1518 CRC64;

Query Match
Best Local Similarity 6.1%; Score 183; DB 1; Length 1007;
Matches 156; Conservative 85; Mismatches 238; Indels 248; Gaps 38;

QY 31 SATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSD----- 77
Db 227 SPTDKSSLLAFL--SNPNTKAKMLEHSGHLVFIDTRSSFIFVPNGNWDQVCSMKVQNGK 284
QY 78 -KEGTGEKEKVEE-----NSDWAVYFNEKGVLTAREITLKAGDNL----- 116
Db 285 TKEDLGLKD-LEDCAKECTGYNKFFSSDWG---NRVDPLVSSKAGIESGGHLPSSVIINN 340
QY 117 -----KIKQGNFTYSL--KKDLTDLTSV--GTEKLSFSANGKNV-----ITS 157
Db 341 KERTCVAYGPNPKENGPNYTPSAWRGRHVRDFGKIFDGT-----APFNKINWSSPTP 394
QY 158 DTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLNLTGAT-TNVTNDNVTDDKKRAASVK 216
Db 395 GDDGISFNETIGSEFPATPPSSPSQTPVINVNVGTVNIGDTNVS----- 443
QY 217 DVLNAGWNIKGVPKT-TASDNVDFVRTYDTVEFLSADTKT---TTVNVESKDNGKKTEV 272
Db 444 -----KG--SGTPTSSQSDM--STDTSDLTSDIDTNNQTNQDINTDNNNSNVDG 490
QY 273 KIGAKTSVIKEKG---KLVTGKDK-----GKNGK-----GENG 298
Db 491 SLSDVDSRVEDDDGVSDTESTNGDSGKTTSTEENGDPSPGDILAAVRKKHLDTVYPGENG 550
QY 299 SSTDEGEGLVTAKE----VIDAVNKAGWRMKTITANGQTGOADKFETVTSGTNVTFAAGK 354
Db 551 GST---EGPLPANQNLGNVIHDVEQNGSAKETIITPGDTGPTDSSSSVDADADVEDTS-- 605
QY 355 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVI----- 405
Db 606 DTDSGIGDDD-----GVSDTESTNG--NNSGKTTSTEENGDPSPGDILAAVRKKHLD 654
QY 406 ----SGNVSPSKGMDERTVINAGNNI-EITRNGKNIDIATSMTP-----QFSSVSLGAG 455
Db 655 TVYPGENGSTEGPL--PANQNLGNVIHDVEQNGAAQE--TIITPGDTESTDTSVVNAN 710
QY 456 ADAPTLS-----VDGDALNVGSKKDKNPV-----RITNVAP 486
Db 711 ADLEDVSDADSGFGDDGSDTESTNGDSGKNTVPDGGTSPGPDILAAVRKKHLDTVYP 770
QY 487 GVKEGDTVNVAQLKGVAQNLNRRIDNVGDNA-----RAGIAQAIATAGLVQAYLP 536
Db 771 GENGSTERPLPAN---QNLGDIHDVEQNGSAKETVVSYPYRGGGGNTSSPIGLA-SLLP 826
QY 537 -----GK-----SMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTAS---- 574
Db 827 ATPSTPLMTTPRTNGKAAASSLMIKGETQA-----KLVKNGGN--IPGETTLAEL 875
QY 575 -GNSRGH 580
Db 876 LPRLRGH 882

RESULT 13
HXA3_HAEIN
ID HXA3_HAEIN STANDARD; PRT; 917 AA.
AC P45355;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
```

```
DE protein A).
GN HXUA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTHI N182;
RX MEDLINE=95115556; PubMed=7815944;
RA Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
RA Mueller-Eberhard U., Hansen E.J.;
RT "The 100 kDa haem:haemopexin-binding protein of Haemophilus
RL influenzae: structure and localization.";
RL Mol. Microbiol. 13:863-873(1994).
CC -!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U08349; AAA74139.1; -.
KW Transport; Signal; Repeat.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 917 HEME/HEMOPEXIN-BINDING PROTEIN.
FT DOMAIN 24 38 3 X 5 AA TANDEM REPEATS.
FT REPEAT 24 28 1-1.
FT REPEAT 29 33 1-2.
FT REPEAT 34 38 1-3.
FT DOMAIN 111 668 6 X 6 AA APPROXIMATE REPEATS.
FT REPEAT 111 116 2-1.
FT REPEAT 203 208 2-2.
FT REPEAT 277 282 2-3.
FT REPEAT 399 404 2-4.
FT REPEAT 624 629 2-5.
FT REPEAT 663 668 2-6.
FT DOMAIN 159 170 2 X 6 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 159 164 3-1.
FT REPEAT 165 170 3-2.
SQ SEQUENCE 917 AA; 100148 MW; 7FF39BB8C046539D CRC64;

Query Match
Best Local Similarity 6.1%; Score 182; DB 1; Length 917;
Matches 119; Conservative 92; Mismatches 223; Indels 124; Gaps 23;

QY 65 VQRTVAVLIVNSDKEGTGEKEKVE--ENSDWAVYFNEKGVLTAREITLKAGDNLKI---K 119
Db 59 INQTSDKVQINWHSFDIGONKEVEFEKQPSSENSVAYNRVTGGNASQIQGKLTANGKVYLAN 118
QY 120 QNGTNFTYSLKKDLTDLTSLVGTTEKLSFSANGKNVNITSDTKGLNFAKETAGTN-----GD 174
Db 119 PNGVIITKGAEinVAGLLATTKDLEQISENSNSYQFTRKTDROVVKEGQVINEGETKAK 178
QY 175 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGTTA 234
Db 179 DFVVLNG-----DEVINKG-----NINV---EKNSTINGKVYLSSGYNFT-----FTL 218
QY 235 SDNVDVVRTYDTVEFLSADTKTTTVN--VESKDNGKKTVEKIGAK----- 277
Db 219 SDS-----GISVALEDNTVRGIVQNEGSIKAGEITLSAKGRKEALDSLVMNGV 267
QY 278 --TSVIKEKDGKLVTKDKGE--NGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTG 334
Db 268 LEATKVSNRNGKVVLSDADNVQLNNEESNIKGEIVNFGTEVTSNEDK---KLKITSKTGSKV 324
QY 335 QADKFETVTSGTNVTFAAGKGTATVSKDDQGNITVMYDVNVGDALNVNQLQN-SGWNLD 393
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Db 325 TSPKINFKGKSVNINGFNGRENSGTHYNEERKTLNTEVNDVPGAENIRIADKDNTETD 384  
QY 394 S-----KAVAGSSGKV-----ISGNVS-----PSKGMD-ETVNINA 424  
Db 385 SFIQTEALSSLLANNGKVNKLGNDVNSIGNINIDSFRTGDSLLKLTNQGHINIDHADINS 444  
QY 425 -GNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDKNKPVRIT- 482  
Db 445 KGRLEFVVTSLQNDVDFKSNITITDSKINLNGAMGLGRSVNEDDYATRWKRAEKSQRKKF 504  
QY 483 NVAPGVKEGDTNVNAQLKGVAQNLNNRIDNV---DGNARAGTAAQAIATAGLVQAYLPKGS 539  
Db 505 NV-----DMRNV-----VFNOQDEVILAGGFEKVNLDKIVAT-----GQT 539  
QY 540 MMAIGGGTYRGEAGYAIG 557  
Db 540 NPYIDGGVSRNRSRYEYG 557

RESULT 14  
OMP\_B\_RICJA STANDARD; PRT; 1656 AA.  
AC 006653;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
DE (rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein  
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).  
GN OMPB.  
OS Rickettsia japonica.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=35790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YH;  
RA Uchiyama T.;  
RT "Sequencing of the gene encoding the protein rOmp B of Rickettsia  
japonica";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
CC SIMILARITY).  
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AB003681; BAA20138.1; .  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; S-layer; Cell wall.  
FT CHAIN 1 1338 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1339 1656 32 KDA BETA PEPTIDE.  
FT DOMAIN 528 533 POLY-GLY.  
SQ SEQUENCE 1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;

Query Match 6.0%; Score 181; DB 1; Length 1656;  
Best Local Similarity 21.9%; Pred. No. 0.11;  
Matches 159; Conservative 80; Mismatches 284; Indels 202; Gaps 35;

QY 10 NSALNAWVAVSELT-----RNHTKRASATV---KTAVLATLLFATVQASANNEEQEE 58  
Db 95 SNANNAVTVSEDTLGLFINNAANRNFNLTDAGKTLTITGOGITNVQSAATHN--- 150  
QY 59 DLYLDPVQRTVA-----VLIVNSDKEGTGEKEKEVEENSDWAVFNEKGVLTAREITLKAG 113  
Db 151 -----AQNVAKFNGGAAIANNDLSGLG---TIDFGAAAATLVFDLANPTTQKAPLILA 201  
QY 114 DNLKIKONGTNETYSLLKDLTDLTSVGTETKLSFSANGKNVNITSDTKGLNFAKETAGTN- 172  
Db 202 DNALI-VNGANGTINVNGFIQVSD-----KSF-ATVKAINI-GDQGFMTNATNANA 253  
QY 173 -----GDTTVHLNGIGSTLTDTLLN-TGATTNVNDNVTDDEKKRAASVKDVLNAGWNK 226  
Db 254 LNLQAGGTTINFNGTGTGRLVLLSKNGAATDF---NVTG-----SLGGLNK 297  
QY 227 GVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVN-----YESKDNKGKTEV--KIGA 276  
Db 298 GIELNTVAINGQLIANAG-----PANAVIGTNNGAGRAAGFVVVDNGKAATIDGQVYA 352  
QY 277 KTSVIKE-----KDGKLVTKGDKGENSGSSTDEGE--GLVTAK 311  
Db 353 KDMVIOANANGQVNFHIVDVGIDGTAFKTAASIVAITQNSFGTTDFGNLAAQVTVP 412  
QY 312 EVIDAV-----NKAGWRMKTTTTANG--QTQADKFEFVTSGTNVTFASGKGT-- 356  
Db 413 DTMTLTGNFTGDANNPGNTAG--VITFAANGTLASASADANAVTNNTITAIEASGVGVWQ 470  
QY 357 -----TATVSKDDQGNITVMYDVNVGDALN--VNQLONSGWNLDKAVAGSSKVISGNV 409  
Db 471 LSGHTAELRLGNAGSVFKLAD--GTVINGKNQTVLVGGVLAAGAITLDGSAITIGDI 527  
QY 410 SPSKG-----KMDETVNINA-GNNIEITRNGKNI---D 438  
Db 528 GNGGGGAALQSITLANDATKTLTLGGANIISANGGTINFQANGGTIKLTSTQNINVVD 587  
QY 439 IATSMTPQFSSVSLGAGADAPTLSDVG-----DALNVGSKK---DNKPVRTN 483  
Db 588 LAIA-TDQTVGVVDASSLTNAQTLTISGTIGIGANNNTTLGQFNIGSSKTTLNGGNVAIN 646  
QY 484 VAPGVKEGDV-----TNVAQLKGVAQNLNNRIDNVGNARAGIAQAIATAGLVQAY 534  
Db 647 LVIG-NNGSVQFAHTYLIIRTTNAAGQKTIFFNVVNNNTTLAAGTNLGSAAANPLAEIN 705  
QY 535 LPGK-----SMMAIGGGTYRGEAGYA-----IGYSSISDGGNWIKGTASGNSRGH 580  
Db 706 FGSKGARADTVLNVGEGVNL---YATNITTDANVGSFVFENAGGNIVSGTVGGQQGNK 761  
QY 581 FGASA 585  
Db 762 FNTVA 766  
RESULT 15  
HX\_A2\_HAEIN STANDARD; PRT; 928 AA.  
AC P45354;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization  
protein A).  
GN HXDA.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 22-35.  
RC STRAIN=DL42 / SEROTYPE B;  
RX MEDLINE=95115556; PubMed=7815944;  
RA Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:30:29 ; Search time 55.9 Seconds  
(without alignments)  
1828.980 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
Sequence: 1 MNKIYRIIWNLSALNAWAVS.....TASGNSRGHFGASASVG YQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2999	99.9	591	16 Q9JRL8	Q9jrl8 neisseria m
2	2995	99.7	591	2 Q9JPS7	Q9jps7 neisseria m
3	2980	99.2	591	2 Q93QY3	Q93qy3 neisseria m
4	2967.5	98.8	592	2 Q9AQF0	Q9aqf0 neisseria m
5	2889.5	96.2	590	2 Q9JPS3	Q9jps3 neisseria m
6	2762.5	92.0	594	2 Q93QY4	Q93qy4 neisseria m
7	2757.5	91.8	600	2 Q9JPS6	Q9jps6 neisseria m
8	2751.5	91.6	594	2 Q9JPI3	Q9jpi3 neisseria m
9	2747.5	91.5	594	2 Q9JPS2	Q9jps2 neisseria m
10	2736.5	91.1	594	2 Q9JPH7	Q9jph7 neisseria m
11	2734.5	91.1	598	2 Q9JPR9	Q9jpr9 neisseria m
12	2721.5	90.6	598	2 Q9JPT0	Q9jpt0 neisseria m
13	2721.5	90.6	598	2 Q9JPS0	Q9jps0 neisseria m
14	2712.5	90.3	598	2 Q93QY5	Q93qy5 neisseria m
15	2689	89.5	599	2 Q9JPR8	Q9jpr8 neisseria m
16	2620.5	87.3	592	2 Q9JPS9	Q9jps9 neisseria m

17	2607	86.8	599	2 Q9JPS8	Q9jps8 neisseria m
18	2578.5	85.9	598	2 Q9JPR7	Q9jpr7 neisseria m
19	2577.5	85.8	592	2 Q93QY2	Q93qy2 neisseria m
20	2528	84.2	595	2 Q9JPH0	Q9jph0 neisseria m
21	2524.5	84.1	600	2 Q9JPS5	Q9jps5 neisseria m
22	2486	82.8	589	2 Q9JPI0	Q9jpi0 neisseria m
23	2475	82.4	589	2 Q93QY1	Q93qy1 neisseria m
24	2468.5	82.2	592	16 Q9JQW4	Q9jqw4 neisseria m
25	2449.5	81.6	526	2 Q9JPS4	Q9jps4 neisseria m
26	2447.5	81.5	530	2 Q9JPS1	Q9jps1 neisseria m
27	1243	41.4	2353	2 P71401	P71401 haemophilus
28	1057.5	35.2	1098	2 Q48152	Q48152 haemophilus
29	435.5	14.5	1299	16 Q9F3X6	Q9f3x6 pasteurella
30	393	13.1	2059	16 Q9PD50	Q9pd50 xylella fas
31	378	12.6	1107	2 Q9F2D8	Q9fd28 salmonella
32	371.5	12.4	1190	16 Q9PC04	Q9pc04 xylella fas
33	368.5	12.3	2712	16 Q9F3X5	Q9f3x5 pasteurella
34	250	8.3	1291	16 Q92KQ7	Q92kq7 rhizobium m
35	243	8.1	1953	16 Q98HJ2	Q98hj2 rhizobium l
36	240.5	8.0	1004	16 Q9PD63	Q9pd63 xylella fas
37	236	7.9	1265	2 Q9FDA0	Q9fda0 xanthomonas
38	235.5	7.8	1039	2 Q9L6T7	Q9l6t7 escherichia
39	235.5	7.8	1040	2 Q9AL50	Q9al50 shigella fl
40	233.5	7.8	2276	2 Q93TY6	Q93ty6 staphylococ
41	232.5	7.7	1536	2 Q48031	Q48031 haemophilus
42	231	7.7	832	2 O54356	O54356 moraxella c
43	229.5	7.6	3930	16 Q98E20	Q98e20 rhizobium l
44	228	7.6	1557	2 Q9RNI2	Q9rni2 haemophilus
45	226.5	7.5	1039	2 Q9L6T8	Q9l6t8 escherichia

ALIGNMENTS

RESULT 1

Q9JRL8					
ID	Q9JRL8	PRELIMINARY;	PRT;	591	AA.
AC	Q9JRL8;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).				
DE	GNA992 OR NMB0992 OR NHHA.				
GN	Neisseria meningitidis, and				
OS	Neisseria meningitidis (serogroup B).				
OS	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487, 491;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;				
RA	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";				
RL	Science 287:1816-1820(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MC58 / SEROGROUP B;				
RX	MEDLINE=20175755; PubMed=10710307;				
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,				







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RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match          96.2%; Score 2889.5; DB 2; Length 590;
Best Local Similarity 97.1%; Pred. No. 7.3e-114;
Matches 575; Conservative 4; Mismatches 10; Indels 3; Gaps 2;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRSATVKTAVLATLLFATVQASANNEEEDL 60
Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRSATVKTAVLATLLFATVQASANNEEEDL 60
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
Db 60 -LDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 118
QY 121 NGTNFTYSLKKDLTSLVSGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 180
Db 119 NGTNFTYSLKKDLTSLVSGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 178
QY 181 GIGSTLTDLTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 240
Db 179 GIGSTLTDLTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 238
QY 241 VRTYDVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGKGENGSS 300
Db 239 VRTYDVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGKGENGSS 298
QY 301 TDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSGTNVTFFASGKGTATV 360
Db 299 TDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSGTNVTFFASGKGTATV 358
QY 361 SKDDQGNITVYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKMDETV 420
Db 359 SKDDQGNITVYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKMDETV 418
QY 421 NINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDNKPV 479
Db 419 NINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNKPV 478
QY 480 RITNVAPGVKEGDVTVNAQLKGVAQNLRNIDNVNVDGNARAGIAQAIAATAGLVQAYLPKGS 539
Db 479 RITNVAPGVKEGDVTVNAQLKGVAQNLRNIDNVNVDGNARAGIAQAIAATAGLVQAYLPKGS 538
QY 540 MMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASNSRGHFGASASVGYQW 591
Db 539 MMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASNSRGHFGASASVGYQW 590

RESULT 6
Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
```

```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=EG327;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
SQ SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;

Query Match          92.0%; Score 2762.5; DB 2; Length 594;
Best Local Similarity 92.5%; Pred. No. 1.5e-108;
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRSATVKTAVLATLLFATVQASANNEEEDL 60
Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRSATVKTAVLATLLFATVQASTTD---DDDL 57
QY 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
Db 58 YLEPVQRTAVVLSFRSDEKGTGEKE-VTEDSNWGVYFDKGVLTAGTITLKAGDNLKIQ 116
QY 121 -----NGTNFTYSLKKDLTSLVSGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 174
Db 117 NTNENTNASSFTYSLKKDLTSLVSGTEKLSFANGKNVNTSDTKGLNFAKKTAAETNGD 176
QY 175 TTVHLNGIGSTLTDLTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKVKPGTTA 234
Db 177 TTVHLNGIGSTLTDLTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNIKVKPGTTA 236
QY 235 SDNVDFVRTYDVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGDK 294
Db 237 SDNVDFVRTYDVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGDK 296
QY 295 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSGTNVTFFASGK 354
Db 297 GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFETVTSGTNVTFFASGK 356
QY 355 GTTATVSKDDQGNITVYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
Db 357 GTTATVSKDDQGNITVYDVNVDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 415 KMDETIVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473
Db 417 KMDETIVNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSK 476
QY 474 KDNKPVRTITNVAPGVKEGDVTVNAQLKGVAQNLRNIDNVNVDGNARAGIAQAIAATAGLVQA 533
Db 477 DANKPVRTITNVAPGVKEGDVTVNAQLKGVAQNLRNIDNVNVDGNARAGIAQAIAATAGLVQA 536
QY 534 YLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASNSRGHFGASASVGYQW 591
Db 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASNSRGHFGASASVGYQW 594

RESULT 7
Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
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RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,	
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,	
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
RA	Moxon E.R., Grandi G., Rappuoli R.;	
RT	"Identification of Vaccine Candidates Against Serogroup B	
RT	Meningococcus by Whole-Genome Sequencing.";	
RL	Science 287:1816-1820(2000).	
DR	EMBL; AF226371; AAF42520.1; -.	
SQ	SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;	
Query Match 91.8%; Score 2757.5; DB 2; Length 600;		
Best Local Similarity 91.5%; Pred. No. 2.5e-108;		
Matches 550; Conservative 14; Mismatches 26; Indels 11; Gaps 3;		
QY	1 MNKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANN---EEQ 56	
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QY	57 EEDLYLDPVQRTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNL 116	
Db	61 EEEYLEPVVRTAPVLSFYSDAEDTGEKE-VTENTNWGIYFDKNGVIKAGTITLKAGDNL 119	
QY	117 KIKQ-----NGTNFTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKETAG 170	
Db	120 KIKQNTDENTNASSFTYSLKKELTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKETAG 179	
QY	171 TNGDTTVHLNGIGSTLTDTLTLLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVP 230	
Db	180 TNGDTTVHLNGIGSTLTDTLTLLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVP 239	
QY	231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVLT 290	
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QY	291 GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350	
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QY	351 ASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVS 410	
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QY	411 PSKGKMDETVNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNV 470	
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QY	471 GSKKDNKPVRIITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGDGNARAGIAQAIAATAGL 530	
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QY	531 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGQ 590	
Db	540 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGQ 599	
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Db	600 W 600	
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AC	Q9JPI3;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	OUTER MEMBRANE PROTEIN GNA992.	
OS	Neisseria meningitidis.	
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	

OX	NCBI_TaxID=487;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NG3/88, AND BZ232;	
RX	MEDLINE=20175756; PubMed=10710308;	
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,	
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,	
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
RA	Moxon E.R., Grandi G., Rappuoli R.;	
RT	"Identification of Vaccine Candidates Against Serogroup B	
RT	Meningococcus by Whole-Genome Sequencing.";	
RL	Science 287:1816-1820(2000).	
DR	EMBL; AF226376; AAF42525.1; -.	
DR	EMBL; AF226369; AAF42518.1; -.	
SQ	SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;	
Query Match 91.6%; Score 2751.5; DB 2; Length 594;		
Best Local Similarity 92.1%; Pred. NO. 4.4e-108;		
Matches 551; Conservative 13; Mismatches 23; Indels 11; Gaps 4;		
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QY	121 -----NGTNFTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKETAGTNGD 174	
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QY	175 TTVHLNGIGSTLTDTLTLLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVPGTTA 234	
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QY	235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGLVTGDK 294	
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QY	415 KMDETVNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473	
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QY	474 KDNKPVRIITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGDGNARAGIAQAATAGLVQA 533	
Db	477 DANKPVRIITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGDGNARAGIAQAATAGLVQA 536	
QY	534 YLPKSKMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 591	
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AC	Q9JPS2;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	OUTER MEMBRANE PROTEIN GNA992.	







QY	534	YLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW	591
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DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NGH36;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.";		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226382; AAF42531.1; -.		
SQ	SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;		
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Best Local Similarity 91.4%; Pred. No. 2.3e-107;			
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QY	171	TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKP	230
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QY	231	GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGLVT	290
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Db	297	GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFEFVTSGTNVTF	356
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QY	411	PSKGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALN	469
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QY	470	VGSKKDNKPVRIITNVAPGVKEGDTVNVAQLKGVQAQNLNNRIDNV DGNARAGIAQAIATAG	529

Db	477	VGSKDTNKPVRITNVAPGVKEGDTVNVAQLKGVQAQNLNNRIDNV DGNALAGIAQAIATAG	536
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Db	537	LVQAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGY	596
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Db	597	QW 598	
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DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=2996;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.";		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226359; AAF42508.1; -.		
SQ	SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;		
Query Match 90.6%; Score 2721.5; DB 2; Length 598;			
Best Local Similarity 90.7%; Pred. No. 8e-107;			
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;			
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Db	1	MNKIYRIIWNALNAWVVSELTRNHTKRASATVATAVALATLLFATVQANATD---DDDL	57
QY	61	YLDPVQRTAVVLIVNSDKEGTGEKEKEVEENS DWAVFNEKGVLTAREITLKAGDNLKIKQ	120
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QY	121	-----NGTNFTYSLKKDLTDLTSVGTEKLSFSAANGKNVNITSDTKGLNFAKETAG	170
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QY	171	TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKP	230
Db	177	TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKP	236
QY	231	GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGLVT	290
Db	237	GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGLVT	296
QY	291	GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFEFVTSGTNVTF	350
Db	297	GKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFEFVTSGTNVTF	356
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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:46 ; Search time 25.63 Seconds  
(without alignments)  
563.228 Million cell updates/sec

Title: US-09-700-293-4  
Perfect score: 3003  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_AA:\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2999	99.9	591	US-09-377-155-21	Sequence 21, Appl
2	2999	99.9	591	US-09-377-155-21	Sequence 21, Appl
3	2980	99.2	591	US-09-377-155-11	Sequence 11, Appl
4	2980	99.2	591	US-09-377-155-11	Sequence 11, Appl
5	2967.5	98.8	592	US-09-377-155-2	Sequence 2, Appl
6	2967.5	98.8	592	US-09-377-155-2	Sequence 2, Appl
7	2762.5	92.0	594	US-09-377-155-9	Sequence 9, Appl
8	2762.5	92.0	594	US-09-377-155-9	Sequence 9, Appl
9	2736.5	91.1	594	US-09-377-155-7	Sequence 7, Appl
10	2736.5	91.1	594	US-09-377-155-7	Sequence 7, Appl
11	2721.5	90.6	598	US-09-377-155-13	Sequence 13, Appl
12	2721.5	90.6	598	US-09-377-155-13	Sequence 13, Appl
13	2712.5	90.3	598	US-09-377-155-5	Sequence 5, Appl
14	2712.5	90.3	598	US-09-377-155-5	Sequence 5, Appl
15	2689	89.5	599	US-09-377-155-15	Sequence 15, Appl
16	2689	89.5	599	US-09-377-155-15	Sequence 15, Appl
17	2577.5	85.8	592	US-09-377-155-17	Sequence 17, Appl
18	2577.5	85.8	592	US-09-377-155-17	Sequence 17, Appl
19	2475	82.4	589	US-09-377-155-19	Sequence 19, Appl
20	2475	82.4	589	US-09-377-155-19	Sequence 19, Appl
21	1245	41.5	2411	US-09-268-347-36	Sequence 36, Appl
22	1243	41.4	2353	US-09-377-155-33	Sequence 33, Appl
23	1243	41.4	2353	US-08-913-942-4	Sequence 4, Appl
24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
25	1242	41.4	2354	US-09-268-347-47	Sequence 47, Appl
26	1180.5	39.3	607	US-08-409-995-6	Sequence 6, Appl
27	1180.5	39.3	607	US-08-409-995-6	Sequence 6, Appl

28	1180.5	39.3	607	4	US-08-913-942-6	Sequence 6, Appl
29	1180.5	39.3	1912	1	US-08-409-995-4	Sequence 4, Appl
30	1180.5	39.3	1912	3	US-08-685-467-4	Sequence 4, Appl
31	1070.5	35.6	1094	4	US-09-268-347-32	Sequence 32, Appl
32	1057.5	35.2	1098	1	US-08-409-995-2	Sequence 2, Appl
33	1057.5	35.2	1098	3	US-08-685-467-2	Sequence 2, Appl
34	1057.5	35.2	1098	4	US-09-377-155-32	Sequence 32, Appl
35	1057.5	35.2	1098	4	US-08-913-942-2	Sequence 2, Appl
36	1057.5	35.2	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1057.5	35.2	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1039.5	34.6	658	1	US-08-409-995-5	Sequence 5, Appl
39	1039.5	34.6	658	3	US-08-685-467-5	Sequence 5, Appl
40	1039.5	34.6	658	4	US-08-913-942-5	Sequence 5, Appl
41	995	33.1	679	4	US-08-913-942-15	Sequence 15, Appl
42	995	33.1	679	4	US-09-268-347-26	Sequence 26, Appl
43	752.5	25.1	1004	4	US-09-268-347-30	Sequence 30, Appl
44	741.5	24.7	1002	4	US-09-268-347-24	Sequence 24, Appl
45	696.5	23.2	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-21  
Sequence 21, Application US/09377155  
Patent No. 6197812  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377.155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 591  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 99.9%; Score 2999; DB 4; Length 591;  
Best Local Similarity 99.8%; Pred. No. 6.7e-225;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps

QY	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL	60
Db	1	MNKIYRIIWSALNAWVVSSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL	60
QY	61	YLDPVQRTVAVLIIVNSDKTEGTEKEKEVEENSDWAVYNEKGVLTAREITLKAGDNLKIKQ	120
Db	61	YLDPVQRTVAVLIIVNSDKTEGTEKEKEVEENSDWAVYNEKGVLTAREITLKAGDNLKIKQ	120
QY	121	NGTNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLN	180
Db	121	NGTNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTVHLN	180
QY	181	GIGSLTDLTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF	240
Db	181	GIGSLTDLTLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF	240
QY	241	VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKDKGENGSS	300
Db	241	VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKDKGENGSS	300
QY	301	TDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKEFTVSGTNVTFASGKGTATV	360

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Db 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360  
QY SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETV 420  
Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETV 420  
QY NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDNKPVR 480  
Db 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDNKPVR 480  
QY ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGDNARAGIAQAIATAGLVQAYLPK GSM 540  
Db 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGDNARAGIAQAIATAGLVQAYLPK GSM 540  
QY MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 2  
US-09-669-974-21 Application US/09669974  
; Sequence 21, Application US/09669974  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 99.9%; Score 2999; DB 4; Length 591;  
Best Local Similarity 99.8%; Pred. No. 6.7e-225;  
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
QY 61 YLDPVQRTVAVLIIVNSDKEGTEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
Db 61 YLDPVQRTVAVLIIVNSDKEGTEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGGTTASDNVDF 240  
Db 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGGTTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENGSS 300  
Db 241 VRTYDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360

Db 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360  
QY SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETV 420  
Db 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETV 420  
QY NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDNKPVR 480  
Db 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKDNKPVR 480  
QY ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGDNARAGIAQAIATAGLVQAYLPK GSM 540  
Db 481 ITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGDNARAGIAQAIATAGLVQAYLPK GSM 540  
QY MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591

RESULT 3  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 99.2%; Score 2980; DB 4; Length 591;  
Best Local Similarity 99.3%; Pred. No. 2e-223;  
Matches 587; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
Db 1 MNEILRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEOEEDL 60  
QY 61 YLDPVQRTVAVLIIVNSDKEGTEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
Db 61 YLDPVQRTVAVLIIVNSDKEGTEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFANGKNVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGGTTASDNVDF 240  
Db 181 GIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGGTTASDNVDF 240  
QY 241 VRTYDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENGSS 300  
Db 241 VRTYDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGENGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTSCTNVTFASGKGTATV 360  
QY 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETV 420

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